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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:09:03 ; Search time 14.16 Seconds
(without alignments)
1334.941 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MKRDMTSGAVTFWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1158.5	26.5	859	3	US-09-183-253-2
2	697.5	15.9	332	3	US-09-183-253-4
3	359	8.2	908	4	US-08-855-146-2
4	355.5	8.1	908	3	US-08-823-110-1
5	355.5	8.1	908	3	US-08-604-298-1
6	355	8.1	915	4	US-08-617-785-12
7	355	8.1	922	4	US-08-617-785-14
8	353	8.1	912	4	US-08-617-785-2
9	353	8.1	915	1	US-08-453-862-2
10	353	8.1	915	2	US-08-452-734A-2
11	353	8.1	915	4	US-08-176-401B-2
12	353	8.1	915	5	PCT-US94-14989-2
13	349.5	8.0	912	5	PCT-US91-09422-19
14	328	7.5	879	1	US-08-072-574-6
15	328	7.5	879	1	US-08-486-270-6
16	328	7.5	879	3	US-08-367-264-6
17	327	7.5	872	3	US-08-337-297A-2
18	327	7.5	872	3	US-09-258-523-2
19	321.5	7.4	867	4	US-08-617-785-4
20	313.5	7.2	877	2	US-08-407-875-2
21	311.5	7.1	877	3	US-09-126-280-2
22	302.5	6.9	1180	4	US-08-660-148-2
23	297.5	6.8	1212	4	US-08-660-148-5
24	283.5	6.5	1180	1	US-08-486-270-8
25	283.5	6.5	1180	3	US-08-367-264-8
26	282.5	6.5	1180	1	US-08-072-574-8
27	280	6.4	1056	2	US-08-687-289A-8

28	278.5	6.4	1212	1	US-08-486-270-10	Sequence 10, Appl
29	278.5	6.4	1212	3	US-08-367-264-10	Sequence 10, Appl
30	276.5	6.3	1212	1	US-08-072-574-10	Sequence 10, Appl
31	276	6.3	906	3	US-08-486-270-2	Sequence 2, Appl
32	276	6.3	906	3	US-08-367-264-2	Sequence 2, Appl
33	276	6.3	1194	4	US-08-538-526-1	Sequence 1, Appl
34	275.5	6.3	905	1	US-08-072-574-2	Sequence 2, Appl
35	273	6.2	1056	2	US-08-687-289A-7	Sequence 7, Appl
36	268	6.1	906	5	PCT-US91-09422-17	Sequence 17, Appl
37	268	6.1	1199	1	US-08-041-538-2	Sequence 2, Appl
38	268	6.1	1199	1	US-08-463-642-2	Sequence 2, Appl
39	268	6.1	1199	1	US-08-455-602-2	Sequence 2, Appl
40	268	6.1	1199	2	US-08-465-157-2	Sequence 2, Appl
41	268	6.1	1199	5	PCT-US91-09422-2	Sequence 12, Appl
42	265.5	6.1	877	1	US-08-486-270-12	Sequence 12, Appl
43	265.5	6.1	877	3	US-08-367-264-12	Sequence 12, Appl
44	263.5	6.0	877	1	US-08-072-574-12	Sequence 12, Appl
45	243	5.6	1058	2	US-08-687-289A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-183-253-2
; Sequence 2, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-183-253-2

Query Match 26.5%; Score 1158.5; DB 3; Length 859;
Best Local Similarity 31.8%; Pred. No. 8.5e-109;

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Matches 268; Conservative 158; Mismatches 296; Indels 121; Gaps 19;
Qy 18 LCLIASPHLQGVAGRP-----DELHIGIPPI---AGKGWQGGQACMPATRLALDDV 68
Db 16 LLLPLAPGAWGARGAPRPPSPPLSLMGLPLTKREVAKGSII--GRGVLPVELAIEQI 73
Qy 69 NKQPNLLPGFKLILHSNDECEBPGILGASVYNNLLYNKPKMLLAG-CSTVCTTVAEAK 127
Db 74 RNESLLRPFY-LDLRLYDFECNAGKAKAFYDAIKYGNHLMVFGVCPSVTSIIAESLQ 132
Qy 128 MNNLLVLCYGASSPALSADKREPTLFTTHPSATVHNPTRIKLMKFGWSRVAILQAAEEV 187
Db 133 GNNVLQSFAPATTPVLADKKKPYFRTVPSDNVNPAILKLLKHQWKRVGTLTQOVQR 192
Qy 188 FISTVEDLENRCMEAGVEIVTQSFSLSDPTDAVRNLRQDARIIVGLFYVVAARRVLCME 247
Db 193 FSEVRNDLTGVLYGEDIEISDFESFNDPCTSVKLLKGNDRVRIILGQFDQONMAAKVFC-- 250
Qy 248 YKQQLYGRAHVWFYFGWYEDNWEVNLKAEGITCTVQEQMRIAEEGHLTTEALMWNQNNQT 307
Db 251 -----CTPQQ-----YEREYNN 262
Qy 308 TISGMTAEERHRLNQALETGVDYINHDYRPEGYQEAFLAYDAVWSVALAFNKTMERL-- 365
Db 263 KRSGVGPSKF-----HGY-----AYDGIWIAKTQLRAMETLHA 296
Qy 366 TTGKSLRDLFTYTDKEIADEIYAAMNSTQFLGSGVYAFSSQGDRIALTQIEQMIDGKYE 425
Db 297 SSRHQRIQDFNTDHTLGRILLNAMNETNFFGTGVQVVRN-GERMGTIKFTQFQDSREV 355
Qy 426 KLGYYDTQLDNLWSLN-TEQWITGKGVQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAF 484
Db 356 KYGEYNADVTLEIINDTIRFQSGEPPKDKTIILEQLRKISLPLYSILSALTILGIMMAS 415
Qy 485 ALIIEINWKRHRVIOSSHVPVNTIMLFGVILICISVILLGIDGRFVSPEEYKICOARA 544
Db 416 AFLFNKRNKRLIKMSSPYMNNLILGMLSYASIFLFGLDGSFVSEKTFETLCVTRT 475
Qy 545 WLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKKKVEPWKLYTMVSGLLSIDLVILLSWQ 604
Db 476 WILTGYTTAFGAMFAKTRVHAIFNVKM-KKKIKDKQLLVIVGGMLLIDILICILCWQ 534
Qy 605 IFDPLQRYLETIPLE--DPVSTTDDDIKIRPELEHCESSQNRSMWGLVYGFGLILVFLGLF 663
Db 535 AVDPLRLRTVEKYSMEPDAGR--DISIRPLEHCENTHMTIWLGIYVAYKGLMLFGCFL 592
Qy 664 AVETRSIKVQINDSRVYVGMSTYNNVVLCITAPVGMVIAASQODASFAFVALAVIFCCFL 723
Db 593 AWETRNVSPALNDSKYIGMSVYVNGIMCIIGAASFLTRDQPNVQFCIVALVIFCGSTI 652
Qy 724 SMLLIFVPKVIEWIRHP-----KDAESKYNPD-SATSKEDDEERYOKLVT 768
Db 653 TILCFVPLKILTRNPDAATQNRERQFTQNKQKEDSKTSVTSVNOASTSRLEGLOSE 712
Qy 769 NEQOLRLITQKEEKIRVLQRRLVERGDAKT-----ELNGATGVASAAVATTSOPAS 820
Db 713 NHRLRMKITELDKDLEEVMTQLQDTP-KTTYIKQNHQYQELNIDILNIGNFTSTDGKAI 771
Qy 821 LIN 823
Db 772 LKN 774
RESULT 2
US-09-183-253-4
; Sequence 4, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSO for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-253-4
Query Match 15.9%; Score 697.5; DB 3; Length 332;
Best Local Similarity 41.4%; Pred. No. 1.7e-62;
Matches 135; Conservative 74; Mismatches 110; Indels 7; Gaps 6;
Qy 372 LRDTYTDKEIADFIYAAMNSTQFLGSGVYAFSSQGDRIALTQIEQMIDGKYEKLGYD 431
Db 2 IQDFNYTDHTLGRILLNAMNETNFFGTGVQVVRN-GERMGTIKFTQFQDSREVKVEYN 60
Qy 432 TQLDNLWSLN-TEQWITGKGVQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALIIFN 490
Db 61 AVADTLEIINDTIRFQSGEPPKDKTIILEQLRKISLPLYSILSALTILGIMMASAFLEFN 120
Qy 491 IWNKRRVIOSSHVPVNTIMLFGVILICISVILLGIDGRFVSPEEYKICOARAWLLSTG 550
Db 121 IKNRQKLIKMSPPYMNLLILGMLSYASIFLFGLDGSFVSEKTFETLCVTRWILVIG 180
Qy 551 FTLAYGAMFSKVRVHRFTTKAKTDPKKKKVEPWKLYTMVSGLLSIDLVILLSWQIFDPLQ 610
Db 181 YTTAFGAMFAKTRVHAIFNVKM-KKKIKDKQLLVIVGGMLLIDILICILCWQAVDPLR 239
Qy 611 RYLETFPLE-DPVSTTDDDIKIRPELEHCESSQNRSMWGLVYGFGLILVFLGLAYERS 669
Db 240 RTVEKYSMEPDAGR--DISIRPLEHCENTHMTIWLGIYVAYKGLMLFGCFLAWETR 297
Qy 670 IKVQINDSRVYVGMSTYNNV-VVLCI 694
Db 298 VSPALNDSKYIGMSVYVNGIISRI 323
RESULT 3
US-08-855-146-2
; Sequence 2, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
```

APPLICANT: Wu, Su
TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Department
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,146
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,243
FILING DATE: 07-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-10836
TELEPHONE: (317) 276-6334
TELEFAX: (317) 276-2764
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-855-146-2

Query Match 8.28; Score 359; DB 4; Length 908;
Best Local Similarity 21.18; Pred. No. 4e-27;
Matches 204; Conservative 153; Mismatches 378; Indels 232; Gaps 44;
QY 13 FWIFLLCLIASPHLQGGVAG-RPD-ELHIGGIFPIAGKGGWGGQAC-----MP 59
DB 22 YWI-LTFMQTHSQEYAHSTRVDGDIILGGLFPVHAG--ERGVPCGELKKEGIHRL 77
QY 60 ATRALDDVKNOPNLLPGFKL---IL-----HNSDSECEPGL 93
DB 78 AMLYDAIDQINKDPDLSNITLGLRDLTCSRDYALEQSLTFVQALIEKSDVKCANGD 137
QY 94 GASVWYLLYNKPKQL-MLLAGSTVCTTVAEAKMWNLVLCYGASSPALSDRKRPPT 151
DB 138 PP-----IFTKPKISGVIGAAASSVIMANILRFKIPQISYASTAPELSDNTRYDF 191
QY 152 LFRTHPSATVHNPRIKLMKFGWSRAVILQQAEEVFSTVEDLENRCME-AGVEIVTRQ 210
DB 192 FSRVVPDSVQAQAMVDIVTALGNWYVSTLASSENGYSGSEVAFQISREIGGVCIASQ 251
QY 211 SFLSDPTDA-----VRNLRQDARIIVGLFVYVAARVLCMEYKQQLYGRAHVWFFIGW 264
DB 252 KIPREPRGPEKTIKRLLETPNARAVIMFANEDDIRILEAAKLNQSGH---FLWIG- 307
QY 265 YEDNW-----YEVNLIKABGICITVEQMRTAAEG---HLTEALMWNQNTTISGMTA 314
DB 308 -SDSWGSKIAPVYQOEIAEAG-AVTILPKRASIDGDFRFSRRTLANNRRV-----WFA 360
QY 315 EEFHRLNQLIERGYDINHDPYEGY-----QEAFLAY--DAVWSVALAFNKT 362
DB 361 EFWEENFGCKLGSGRKRNHSHKCTGLERIARDSYEOGKVQFVIDAVYSNAYALHNMH 420
QY 363 ERLTGTGKSL--RDFVTYDKDEIADEIYVAMNSTOFLGVSGV-VAFSSOGDRIALFOIEQ- 418

DB 421 KDLCPGYIGLCPRMSTIDGKELGYIRA-----VNFNGSACTPVTFNENGADPGRYDIFYQ 476
QY 419 MIDGK---YEKLGYYDTQL-----DNLSQLNTEQWIGKVPQDRTIVTHLVRTVSLP--- 467
DB 477 QITNKSTYKVIQHWITNQLHLKVEDMQWAHREH-----THPASVCSLPCKPG 523
QY 468 -----LFVCMCTI-----SSC----- 478
DB 524 ERKKTGVGPCWCHCERCEGYNYQVDELSCELCPLDQRPNNRNTGCQOLIPIKLEHSPW 583
QY 479 ---GIFVA-----FALLIENIWNKHRVIOSSHVPVCNTIMLFGVILCLISVILLGID 527
DB 584 AVVPFVAILGIATTFVIVTFVRYN-DTPIVRASGRELSYVLLTGIFLCYSITFLM--- 639
QY 528 GREVSPEEYKIQCARAWLLSTGTFLAYGAMFSGKVMRVHRFTTKAK---TDPKKKVEPMK 584
DB 640 --IAAPDTI--ICSFRVFLGCMCFPSYAALLTKTNRIHRIFEQGKKSVTAP-KFISPAS 694
QY 585 LYTMSGLLSIDLWISWOIFDPLQRYLETFFPLEDPVSTDDIKIRPELEHGESQNSM 644
DB 695 QLVITFESLISVQLLGVFWFVDPPIIID-----YGEQRTLDPEKARGVLK-CDISDLSL 749
QY 645 WLGLVYGFKGLILVFLGLFAYETRSIKVKQINDSRVYVMSIYVNVVLCILITAPVGMVIA 704
DB 750 ICSL--GYSILLMVTCTVYANKTRGV-ETFNKAPIGFTMTYTCIWLAFIPIFFGTQA 806
QY 705 QODASE---AFVALAVIFCCFLSMLLIFVPKVIETVRHPKDKAESKYNPDALSKEDEER 761
DB 807 SAEKMYIQTTLTVSMSLSASVSLGMLYMPKVIIIFHPQNVQKR-----KRS 855
QY 762 YQKLVTENEQQLRITQKEEKIRVLRQLVERGDATKTELNGATGVASAAVATTSQFASL 821
DB 856 FRAVVTAAATMQSKLIQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTTY 900
QY 822 INSSAHA 828
DB 901 ISYNSHS 907

RESULT 4
US-08-823-110-1
Sequence 1, Application US/08823110
Patent No. 6077675
GENERAL INFORMATION:
APPLICANT: Stormann, Thomas M.
APPLICANT: Simin, Rachel T.
APPLICANT: Hammerland, Lance G.
APPLICANT: Fuller, Forrest H.
TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
TITLE OF INVENTION: GLUTAMATE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fastseq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,110
FILING DATE: March 24, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/604,298
FILING DATE: February 21, 1996
ATTORNEY/AGENT INFORMATION:


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Db 78 AMLYDAIDQINDPDDLSSNITLGVRLDTCSDRTYALBOSLTFVQALIEKADSDVRCANDG 137
Qy 94 GASVYNLLYNKPKQL--MLLAGCSTVCTTVAEAAKMNLLVLCYGASSPALSDRKRFTPT 151
Db 138 PP-----IFPKDKISGIVAASSVSWANILRLKPIPOISYASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVNPTRIKMKKFGSRVAILOQAEEVFISTVDELENRCME-AGVEIVTRQ 210
Db 192 FSRVVPDPSYQAQAMVDIVTALGVNYSVTLASEGNYGESGVAEFTQISREIGGVCIQAQSQ 251
Qy 211 SFLSDPTDA-----VRNLRQDARIIVGLFVVAARRVLCMEYKQOLYGRAHVFFIGW 264
Db 252 KIPREPRGEPEKLIKRLLETPNARAVINFANEDDIRILEAAKLNQSGH---FLWIG- 307
Qy 265 YEDNW-----YEVNKAEGITCVEQMRTAAEG---HLTTEALMNQNNQTTISGWT 314
Db 308 -SDSWGSKIAPVYQOEAEAG-AVTILPKRASIDGDFRFRSRTLANNRNV-----WFA 360
Qy 315 EEFHRLNQALIEGYDINHRYPEGY-----OEAPLAY--DAVWSVALAFNKT 362
Db 361 EFWEENFCKLGGHGRNSHIKCTGLERIARDSSVEQEGKVQFVIDAVYSNAYALHNNH 420
Qy 363 ERLTGTGKSL--RDTTYTDKEIADBIYAAAMSTQFLGSGV-VAFSSQGDRIALTQIEQ- 418
Db 421 KDLCPGYIGLCPRMSTIDGKELLYIRA---VNFNGSAGTPTVTFNENGADPGRYDIFQY 476
Qy 419 MIDCK---YELGLGYDTOL---DNLSWLNTQEWIGGKVPQDRTIVTVLRTVSLP--- 467
Db 477 QITNKTSEYKIVIGHWTNQLHLKVEDMQWAHREH-----THPASVCSLPCRP 523
Qy 468 -----LFVCMCTI---SSC----- 478
Db 524 ERKKTGVGPCWCHERCEGYNYQVDELSCELCPLDQRPNNMRTGCOLIPIIKLEHSPW 583
Qy 479 ---GIFVA-----FALITINWKNHRRVIOSSHPCVNTIMLPGVILCLISVILLGD 527
Db 584 AVVPFVAILGIIATTFIVITFVRYN-DTPIVRASGRELSYVLLTGIFLCYSITFLM--- 639
Qy 528 GRFVSPPEYKICQARAWLLSTGTLAYGAFESKVVWRHRTTAK---TDPKKKVEPWK 584
Db 640 --IAAPDI--ICSFRRVFLGLGMCFSYAALLTKTNHRIPEQKKSVTAP-KFISPAS 694
Qy 585 LYTMVSGLLSIDLVLISQWIFDPLQRYLETFPLEDPDYSTDIDKIRPELEHCESORNSM 644
Db 695 QLVITFSLISVOLGVFWFVVDPHIID---YGEORTLDPKARGVLK-CDISDLSL 749
Qy 645 WLGLVYGFGLILYFGLFAYETRSIKYKQINDSRVGMYSIYNVVVLCLITAPVGMVIAS 704
Db 750 ICSL--GVSILLMVTCTVYAIKTRGV-ETENEAKEPIGFTMYTTCIWLAFIPIFFGTAQ 806
Qy 705 QODASF---ATVALAVIPCCFLSMILLIIVPKVIEVIRHPKKAESKYNPDSAISKEDEER 761
Db 807 SAEKMYIQTTLTYTMSLSASVSLGMLYMPKVIYIIFHPQNVQR-----RRS 855
Qy 762 YOKLVTENEQRLITOKEEK 782
Db 856 FRVVVTAATMQSKLIQGNDR 876
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RESULT 6

```
US-08-617-785-12
; Sequence 12, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
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; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-12
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Query Match 8.1%; Score 355; DB 4; Length 915;
Best Local Similarity 21.5%; Pred. No. 1e-26;
Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;
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Qy 17 LLCLIA-----SPH---LOGGVAGRDELHIGGIFPIACKGGWOGQAC----- 57
Db 24 LICALAAARGOEMYAPHSTRIEGDT-----LGLFPVHAKG--PSGVPCGDIKREN 74
Qy 58 ---MPATRLALDDVNKQPNLLPGFKL---IL-----HSNDS 87
Db 75 GIHRLLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDYVALBOSLTFVQALIQKDTSDV 134
Qy 88 ECEPGLGASVYNNLLYNKPKMLLAGC--STVCTTVAEAAKMNLLVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVSIMVANILRLFIQIPQISYASTAPELSD 188
Qy 146 RKEPFLFRTHPSATVNPTRIKMKKFGSRVAILOQAEEVFISTVDELENRCMEAGVE 205
Db 189 DRYDFFSRVVPPDSFOQAAMVDIVKALGNW-----YVSTLAS-EGSYGKGV 236
Qy 206 IVTRQSFSLDPTDAVNLR---RQDA-----RIIVGLFVVAARRVLC---EMVKKOOL 252
Db 237 SFTQISKEAGGLCIAOSVRIPQERKDRITDFDRIIKQLDTPNSRAVIFANEDIKQIL 296
Qy 253 YG--RA-HVMFFIGWYEDNW-----YEVNKAEGITCVEQMRTAAEG---HLTTEAL 299
Db 297 AAAKRAQVGHFLWVGSDSGSKINPLHQHEDIAEG-AITIQPKRATVEGDFAYFTSRTL 355
Qy 300 -----MW-----NONNOTTISGMTAEF--PHRLNQALIEGYDINHRYPEGVQEAP 345
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTRKCTGOERI--GKDSNYEQ--EG--KVQ 409
Qy 346 LAYDAVWSVALAFNKTMERLT-----GKKSRLDFTYTDKEIADBIYAAAMNS 392
Db 410 FVIDAYAMAHUHHNMKDLCADYRGVCPMEQAGGKKLKK-----YIRN 454
Qy 393 TQFLGVSGV-VAFSSQGDRIALTQIEQMDIGYKELGYDTQDLNLSW-----L 440
Db 455 VNFNGSAGTPVMEKNKG-----APGRYDIFQYQTTNTSNPCYRLIGQWTDLQQL 504
Qy 441 NTE--QWIGG--KVP----- 451
Db 505 NIEDMQWKGVRIPASVCTLPCKGQRKKTQGTGCCWTCPCDGYQYQFDEMTQCHP 564
Qy 452 -----QDRTIVT---HVLFTVSLPFLVCMTCTISSCGIFVAFALIIFNINKHR 496
Db 565 YDQRPNEPRTGQODIPIIKLEWHSWAV-IPVFLAMLGIIAT-IFVMTATFIRYN---DT 618
Qy 497 RVIOSSHPCVNTIMLFGVITCLISVILLGIDGRFVSPEEYKICQARAWLLSTGFTLAYG 556
Db 619 PIVRASGRELSVLLTGIFLCYIITFLM-----IAKPD--VAVCFRRVFLGLCMCISYA 671
Qy 557 AMFSKVVWRHRTTAK---TDPKKKVEPWKLYTMVSGLLSIDLVLISQWIFDLPQRYL 613
Db 672 ALLTKNRIYRIFPEQKKSVTAP-RLISPTISQLAITSSLSVQLLGVFIWFGVDPNPNI 730
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[illegible]

Db 297 AAARADQVGHFLWVSDSGSKINPLHQHEDIAEG-AITIQKRAVTEGFDAYFTSRTL 355
QY 300 -----MW-----NONQFTISGMTAEF-RHRLNQALIEBGYDINHDPYEGYQAP 345
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTDRKCTGOERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVWSVALAFNKTMRLLT-----GKKSIRDFTYDKEADEIYAAMNS 392
Db 410 FVIDAVYAMAHALHMHKNDLCADYRGVCPMEQAGGKLLKYIRHVN----- 456
QY 393 TOFLGVSGV-VAFSSQGDRIALTOIEQMDGKYELGYDQTDNLWS-----L 440
Db 457 --FNGSAGTPVMFNKNGD-----APGRYDFIQYQTTNTNPGYRLIGOWTDELQ 504
QY 441 NTE--QWIGG--KVPO-----DRTIVTH-- 459
Db 505 NIEDMQGKGVREIPSSVCTLPCKPQRRKTKGTGCCWTCPCDGYQYQFDEMTQCHP 564
QY 460 -----VLRT-----VSLPLFCMCTISSCGIFVAFALIFNINWKKHR 497
Db 565 YDQRPENRTGCONIPIIKLEWSPWAVIPVFLAMLGIAT-IFVMTATFIRN-----DTP 619
QY 498 VIQSHPCVNTIMLFGVVICLSVILLIDGRFVSPPEYPKICOARAWLLSTGFTLAYGA 557
Db 620 IVRASGRELSYLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVFLGLGMCISYAA 672
QY 558 MFSKVMVRHFTTAK--TDPKKVEPWKLYTMVSGLLSIDLVLLSQIFDPLQRYLE 614
Db 673 LUTKTRNRYRIFEOGKKSVTAP-RLISPTSQLAITSSLSVQLLGVFWFGVDPNNIID 731
QY 615 TPLEDPVSTDDIKTRPLEHCESSORNSWGLVGVFGKLLVFLGFLAYERSTKVQ 674
Db 732 ----YDEHKTMPQARGVLK-CDITDLQICSL--GYSILLMVTCTVYAIKTRGVP-EN 783
QY 675 INDSRVGMSINVVVLCITAPVGMVIAOQDASFAV-----ALAVIFCCFLSMILLIF 729
Db 784 FNEAKPIGFTMTCTCIWLAIFI--FFGTAQSAEKLYIQTTTLTSMNLSASVALGMLY 841
QY 730 VPKEVIRHPKDKAESKYNPDSAISKEDDEERYQKLVTEQLORLITQKEKIRVLRQR 789
Db 842 MPKVYIIIFHPELNVQKR-----KRSPKAVVTAATMSRSLSHKPSDR----- 883
QY 790 LVERGDAKTEL 801
Db 884 --PNGEAK-TEL 892

RESULT 10

US-08-452-734A-2
; Sequence 2, Application US/08452734A
; Patent No. 5831047
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,734A

; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-1
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-452-734A-2

Query Match 8.1%; Score 353; DB 2; Length 915;
Best Local Similarity 21.2%; Pred. No. 1.7e-26;
Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LCLLIA-----SPH---LQGVAGRPDELHIGGIFPIAGKGGWGGQAC----- 57
Db 24 LLCVLAARAAQEQMAYAPHSIRIEGDVT-----LGGILFPVHAKG--PSGVPCGDIKREN 74
QY 58 ----MPATRLALDDVNKPNLLPGFKL--IL-----HNSDS 87
Db 75 GIHLEAMLYALDQINSNPILLPNVTLGARLDCSRDTYALEOSLTFVQALIGKDSV 134
QY 88 ECEPGLGASVMYLLYNKPKQKMLLAGC--STVCTTVAEAAKMMNLI VLYCAGSPALSD 145
Db 135 RCTNGEPP-----VFVKPKVGVIGAGSGSVSWANILRLQIQISASTAPELSD 188
QY 146 KRREPTLFRTHPSATVNPTRIKLKKFGSRVAILQOAEVFFISTVEDLENRCMEAGVE 205
Db 189 DRRYDFSRVVPDPSFOAQMVDIVKALGN-----YVSTLAS-EGSYGEGKVE 236
QY 206 IVTRQSFSLDPTDAVNLRL---RQDA-----RIIVGLFVYVVAARRVLC-----EMYKQOL 252
Db 237 SFTQISKEAGGLCTAQSVRIPOERKORTIDPDRIKQLLDPNRAVVFANDEDIKQIL 296
QY 253 YG--RA-HVWFFIGWYEDNW-----YEVLKAEGITCTVEQMRIAAEG---HLTTEAL 299
Db 297 AAARADQVGHFLWVSDSGSKINPLHQHEDIAEG-AITIQKRAVTEGFDAYFTSRTL 355
QY 300 -----MW-----NONQFTISGMTAEF-RHRLNQALIEBGYDINHDPYEGYQAP 345
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTDRKCTGOERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVWSVALAFNKTMRLLT-----GKKSIRDFTYDKEADEIYAAMNS 392
Db 410 FVIDAVYAMAHALHMHKNDLCADYRGVCPMEQAGGKLLKYIRHVN----- 456
QY 393 TOFLGVSGV-VAFSSQGDRIALTOIEQMDGKYELGYDQTDNLWS-----L 440
Db 457 --FNGSAGTPVMFNKNGD-----APGRYDFIQYQTTNTNPGYRLIGOWTDELQ 504
QY 441 NTE--QWIGG--KVPO-----DRTIVTH-- 459
Db 505 NIEDMQGKGVREIPSSVCTLPCKPQRRKTKGTGCCWTCPCDGYQYQFDEMTQCHP 564
QY 460 -----VLRT-----VSLPLFCMCTISSCGIFVAFALIFNINWKKHR 497
Db 565 YDQRPENRTGCONIPIIKLEWSPWAVIPVFLAMLGIAT-IFVMTATFIRN-----DTP 619
QY 498 VIQSHPCVNTIMLFGVVICLSVILLIDGRFVSPPEYPKICOARAWLLSTGFTLAYGA 557
Db 620 IVRASGRELSYLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVFLGLGMCISYAA 672


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QY 558 MFSKVRVHRFTTKAK---TDPKKKVPWKLYTWVSGLLSIDLVILLWSQIDFPLORYLE 614
Db 673 LTTKTNRIYRIFEQGKSVTAP-RLISPTSQLAITSSLSVOLLGVFIWFGVDPNIIID 731
QY 615 TFPLEDPVSTDDIKIRPELEHCESSQNSMWLGLVYGFGLILVFLFLAYETRSIKVKQ 674
Db 732 ----YDEHKTMPNPEQARGVLK-CDITDLOIICSL--GYSILLMVTCTVYAIKTRGVP-EN 783
QY 675 INDSRYGMSIYNVVVLCLITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLIF 729
Db 784 FNEAKPIGFTMYTTCIVWLAFIPI--FFGTAQSAEKLYIQTTLTISMLNSASVALGMLY 841
QY 730 VPKVIEVIRHPKDKAESKYNPDSALSKEDEERYQKLVTEQOLRLITQKEKIRVLROR 789
Db 842 MPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSSRLSHKPSDR----- 883
QY 790 LVERGDAKGTEL 801
Db 884 --PNGEAK-TEL 892

RESULT 11
US-08-176-401B-2
; Sequence 2, Application US/08176401B
; Patent No. 6274330
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-401B-2

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Query Match      8.1%; Score 353; DB 4; Length 915;
Best Local Similarity 21.2%; Pred. No. 1.7e-26;
Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LLCUIA-----SPH---LQGVAGRPDELHIGGIFPIAGKGGWGGQAC----- 57
Db 24 LLCVLAARQAQEMVAPHISIRIEGDT-----LGGFLFPVHAKG--PSGVPCGDKIKREN 74

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QY 58 ---MPATRLALDDVNKQPNLLPGFKL---IL-----HSNDS 87
Db 75 GIHRLKAMLYALDQIINSDPNLLPNVLTIGARILDTCSBDTYALEQSLTFVQALLQKDTSDY 134
QY 88 ECEPGLGASVYMLLYNKKPKMLLAGC--STVCTTVAEAAKMWLNLLVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPEKVVGVIGAGSSSVIMVANILRLFIQIPIQIYASTAPELSD 188
QY 146 KRKEPTLFRTHPSATVHNPTRIKLMKFKGSRVAILQQAEEVFISTVEDLENRCMEAGVE 205
Db 189 DREYDFFSRVVPDPSFOQAQAMVDIVRALGN-----YVSTLAS-EGSVGEGKVE 236
QY 206 IVTRQSFSLDPTDAVNLNR-----RQDA-----RIIVGLFVYVAARRVLC-----EMTKQQL 252
Db 237 SFTQISKEAGGLCIAOSVRIPQERKDRITIDFRIIKQLLDTPNRAVIVFANDEDIKQIL 296
QY 253 YG--RA-HWFFFIGWYEDNW-----YEVNLAEGITCTVEQMRIAAG--HLITEAL 299
Db 297 AAARADQVGHFLMWGSDSGSKINPLHQHEDIAEG-AITIQKRAIVEGDFAYFTSRTL 355
QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNQAALIEEGYDINHRYPEGYQEP 345
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKKEDTDRKCTQERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVMSVALAFNKTWERLTT-----GKSLRDFTYTDKEIADEIYAMNS 392
Db 410 FVIDAVYMAHALHMHMKDLCADYRGVCPEMQAGGKKLLKYIRHVN----- 456
QY 393 TQFLGVSGV-VAFSSOGDRIALQIEMIDGKYEKLGYYDTQDNLWS-----L 440
Db 457 --FNGSAGTPVMFNKNGD-----APGRYDIFQYQTTNTNPGYRLIGOWTDELQ 504
QY 441 NTE--QWIGG--KVPO-----DRTIVTH-- 459
Db 505 NIEDMONGVREIPSSVCTLPCKGQKKTQKTPCCWTCPCDGVQYQFDEMTQOHP 564
QY 460 -----VLRT-----VSLPLFVCMCTISSCGIFVAFALIFINWKNHRR 497
Db 565 YDORPNENRTGCONIPIIKLEHSPWAVIPVFLAMLGIAT-IFVMATFIRYN----DTP 619
QY 498 VIOSSHVCNTIMLFGVVICLISVILLGIDGRFVSPPEYKPCOARAWLLSTGFTLAYGA 557
Db 620 IVRASGRELSYVLLTGIFLCYIITFLM-----IAKPD--VAVGSFRVFLGLGMCISYAA 672
QY 558 MFSKVRVHRFTTKAK---TDPKKKVPWKLYTWVSGLLSIDLVILLWSQIDFPLORYLE 614
Db 673 LTTKTNRIYRIFEQGKSVTAP-RLISPTSQLAITSSLSVOLLGVFIWFGVDPNIIID 731
QY 615 TFPLEDPVSTDDIKIRPELEHCESSQNSMWLGLVYGFGLILVFLFLAYETRSIKVKQ 674
Db 732 ----YDEHKTMPNPEQARGVLK-CDITDLOIICSL--GYSILLMVTCTVYAIKTRGVP-EN 783
QY 675 INDSRYGMSIYNVVVLCLITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLIF 729
Db 784 FNEAKPIGFTMYTTCIVWLAFIPI--FFGTAQSAEKLYIQTTLTISMLNSASVALGMLY 841
QY 730 VPKVIEVIRHPKDKAESKYNPDSALSKEDEERYQKLVTEQOLRLITQKEKIRVLROR 789
Db 842 MPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSSRLSHKPSDR----- 883
QY 790 LVERGDAKGTEL 801
Db 884 --PNGEAK-TEL 892

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RESULT 12
PCT-US94-14989-2
; Sequence 2, Application PC/TUS9414989
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14989
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,401
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-18PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14989-2

Query Match 8.1%; Score 353; DB 5; Length 915;
Best Local Similarity 21.2%; Pred. No. 1.7e-26;
Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LCLCIA-----SPH---LOGGVAGRPDELHIGGIPPIAGKGGWGGQAC----- 57
DB 24 LCLVIAAARGOEMVAPHSIRIEGDT-----LGLLFPVHAKG--PSGVPCCGDIKREN 74
QY 58 ----MPATRLADDDVNKPNLLPGFKL--IL-----HSNDS 87
DB 75 GTHREAMLYALDQINSDNLLPNVTLGARILDTCSRDIYVALEQSLTFVQALLQKOTSDV 134
QY 88 ECEPLGASVMYNYLKPQKMLLAGC--STVCTTVAEAKMNLIVLCYGASSPALSD 145
DB 135 RCTNGEPP-----VFVEKVVGVIGAGSSVSIMVNLRLFOIPQISYASTAPELSD 188
QY 146 RRRFPTLFTHSATVHNTRIKMKFGWSRVAILQAAEEVISTVEDLENRCMEAGVE 205
DB 189 DRRYDFFSRVPPDSFQAQAMVDIVKALGN-----YVSTLAS-EGSYGKGV 236
QY 206 IVTRQSFLSDPTDAVNLR-----RQDA-----RIIVGLFVVAARRVLC-----EMYKQQL 252
DB 237 SFTQISKEAGGLCIAQSVRIPOERKORTIDFRIIKOLLDTNPSRAVVIFPANDEDIKQIL 296
QY 253 YG--RA-HVWFFIGWYEDNN-----YEVNKAEGITCTVEQMRTAAEG---HLTTEAL 299
DB 297 AAKRADQVCHFLWGSWSGSKINPLHQHEDTAEG-AITIQKRAVTEGFDAYFTSRTL 355
QY 300 -----MW-----NONQTTISGMTAEF-RHRLNQAIIIEGYDINHRYPEGYQEA 345
DB 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTDRKCTQERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVSWALAFNKMTHERLT-----GKSLRDTFTYDKEITADEIYAAMNS 392
DB 410 FVIDAVYAMAHALHHMKNKDLCADYRGVCPMEQAGKLLKYIRHVN----- 456
QY 393 TOFLGVSGV-VAFSSOGDRIALTQIEQMDGKVEKLYGYDTQDLNLSW-----L 440
DB 457 --FNSAGTPVFNKNGD-----APGRYDIFQYQTNTNPGYRLIGQWTDLQL 504
QY 441 NTE--QWIGG--KVPO-----DRITVTH-- 459
DB 505 NIEDMQMGKGVREIPSSVCTLPCKPGQRKTKGTCCWTCPCDGVQYQFDEMTCHQCP 564
QY 460 -----VLRP-----VSLPLFVCMCTISSCGIFVAFALIFINWKKRR 497

DB 565 YDORPENRTGCONIPIIKLEWSPWAVIPVFLAMLGLIAT-IFVMAFIRYN----DTP 619
QY 498 VIOSHPVCNTIMLFGVILICLSVILLIGDGRFVSPREYKICQARAWLLSTGFTLAYGA 557
DB 620 IVRASGRELSYVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVRFLGCMCISYAA 672
QY 558 MFSKVRVHRFTTKAK--TDPKKKVPKLYTMVSGLLSIDLIVLLSWQIFDPLQRYLE 614
DB 673 LLTKNRIYRIFEGQKKSVTAP-RLISPTQLATSSLSISVQLLGVIWFGVDPPNLIID 731
QY 615 TPLEDPVSTDDIKIRPELEHCHESQSNRMWLGIVYGFGLILVFLGLAYETRSIKVKQ 674
DB 732 ----YDEHKTWNPQARGVLK-CDITDLQIICSL--GVSILLMVTCTVYAIKTRGVP-EN 783
QY 675 INDSRYGMSIYNVVLCLITAPVGMVIAOQDASFAFV-----ALAVIFCCFLSMLLIIF 729
DB 784 FNEAKPIGFTMYTTCIVWLAFIPI--PFGTAQSAEKLYIQTTLTISMNLSASVALGMLY 841
QY 730 VPKVIEVIRHPKDKAESKYNPDSAISKEDEBERYOKLVTENEQLOLRLITOKEEKIRVLRQR 789
DB 842 MPKYVIIIFHPELNVQKR-----KRSFRAVVTAATMSSRLSHKPSDR----- 883
QY 790 LVERGDAGKTEL 801
DB 884 --PNGEAK-TEL 892

RESULT 13
PCT-US91-09422-19
Sequence 19, Application PC/TUS9109422
GENERAL INFORMATION:
APPLICANT: Mulvihill, Eileen R.
APPLICANT: Hagen, Frederick S.
APPLICANT: Houamed, Khaled M.
APPLICANT: Almers, Wolfhard
TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09422
FILING DATE: 19911212
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,007
FILING DATE: 18-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,481
FILING DATE: 30-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,806
FILING DATE: 12-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-6PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 912 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-09422-19

Query Match 8.0%; Score 349.5; DB 5; Length 912;
Best Local Similarity 18.9%; Pred. No. 3.7e-26;
Matches 177; Conservative 165; Mismatches 372; Indels 223; Gaps 37;

QY 5 MTSQGVTFW--IFLLCLIAS-----PHLQGGVAGRP-----DELHIGGIPPIAGK 48
DB 1 MSGKGGWAWWARUPLCLLLSLYAPWVPSSLGKPKGHPHMSIRIDGDTLGLGEPVHGR 60
QY 49 GGWGGQAC-----MPATRLALDDVNKPNLLPGFKL-----80
DB 61 G--SEGRACGELKKEGTHRLLEAMFALDRINNDPDLNPTILGARILDTCSRDTALRQ 118
QY 81 -----ILHNSDSCEPG--LGASVWYVLLNPKPKMLLAGC--STVCTTVAEAAKMN 130
DB 119 SLTFVRALIEKDGTEVRCGRGPPII-----TKPVRVGVIGASGSSVIMVANILRLFK 173
QY 131 LIVCYGASSPALSORKRFTFLFRTHPSATVHNPTRIKLMKFGWSRVAIL-----QQ 183
DB 174 IPOISYASTAPDLSDNSRYDFESRVVPSDTYQAQAMVDIVRAKWNVSTLASESGYGES 233
QY 184 AEEVFISTVEDLENRCMEAGVEIVTRQSFSLSDPTDAVRNLRQDARIIVGLFYVVAARRV 243
DB 234 GVEAFIQSRENGGVCIAQSVKIPREPKTGEPDKIIRKLETNSARGIIFANEDDIRV 293
QY 244 LCEMYKOOLYGRAHWFFIGYEDNW-----YEVNLKAG--ITCTVEQMRIAAGHILT 295
DB 294 LEAARRANQTGH---FFWMG--SDSWGSKSAPVLRLAEVAGAVTILPKRMSVGRDFRYF 348
QY 296 TEALMNQNNQTTISGMTAEFRHLNQALIEEGYDI---NHDRYPE--GYQE---APL 346
DB 349 SSRTLDNNRNINWAEFWEDHFCKLSRLALKSHIKKCNRRERIGQDSAYEQEGKVOF 408
QY 347 AYDAVWSVALAFNMTMERLTGKKSRLDFTYTDKEIADEIYAAMNSTQFLVSG-VWAFS 405
DB 409 VIDAVYANGHALHMRDLCPGRVCL--CPRMDPDVGQQLLKYIRNVNFSGIAGNPVTN 466
QY 406 SQGRIALTQEQMDGKYELGYDYDTOLDN-----LSW-----LNTEQWIGKV 450
DB 467 ENGQ-----APGRYD---IVQYQLRNGSAEYKVGIVGWSWTDHLRLRIERMQWPGSQ 513
QY 451 PQDRFTVT-----HVLRT-----463
DB 514 QLPRISCSLPCQGERKKTVMGMACCHCEPCTGYQYQVDRYTCKTCYDMRPTENRTSC 573
QY 464 -----VSLPLFCMCTTSSCGIFVAFALIIFNIWNKRRVIOSSHPCVNTI 509
DB 574 QPIPIVKLEWDSWAVLFLFVAVGIAT-LFVVVTFVRYN---DTPIVKASGRELSV 628
QY 510 MLFGVITICLSVILLGIDGRFVSPEEYKPKICOARAWLLSTGFTLAYGAMFKSWRVHRPT 569
DB 629 LLAGIFLCYATFLM-----IAEPD--LGTCSLRRIFLGLGMSISYAALLTKTNIYRIF 681
QY 570 TKAK--TDPKKKVPWKLYTMVSGLLSIDLLISLWQIFDPLQRYLETFPLEDPVSTTDD 627
DB 682 EQGRSVSAPRFISPASOLAITFTLISLQLLGICVWFVVDPSHVVQ---FQD--QRTLD 736
QY 628 IKIRPELHESQSNMVLGVYFGKGLILVFLGLFVAYETRSIKVKQINDSRYVGMVLYN 687
DB 737 PRFARGVLKCDI--SDLSLICLLGYSMLLMTCTVYALKTKGVP-ETNEAKPIGFTMT 793
QY 688 VVVLITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLIFVPKVIETIRHPKD 742
DB 794 TCIWLAFIPI--FFGTSQSAKLYIQTTTLTVSVLSASYSGLMYPKYVILLFHEPQ 851
QY 743 KAESKYNPDSAISKEDEERYOKLVTENEQLORLITQK 779
DB 852 NVPKR-----KRSLLKAVVTAATMSNKFTQK 876

RESULT 14
US-08-072-574-6
; Sequence 6, Application US/08072574
; Patent No. 5521297
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen
; APPLICANT: Pontsler, Aaron
; TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
; NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 00719
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/072,574
; FILING DATE: 19930604
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-622-7700
; TELEFAX: 213-489-4210
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 879 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-072-574-6

Query Match 7.5%; Score 328; DB 1; Length 879;
Best Local Similarity 20.1%; Pred. No. 5.5e-24;
Matches 175; Conservative 134; Mismatches 320; Indels 242; Gaps 36;

QY 36 ELHIGGIFPIAGKGGWGOAC-----MPATRLALDDVNKPNLLPGFKLILHS 84
DB 38 DIVLIGGLFFINEKG--TGTECGRINEDRGIOQLRLFAIDEINKDDYLLPGVKLGVHI 95
QY 85 NDS-----ECPGGLGASVYNNLYNKKPKMLLAGC-- 115
DB 96 LDTCSRDTYALQSLFLEFVRASLTKKVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147
QY 116 ---STVCTTVAEAAKMNLIIVCYGASSPALSORKRFPFLFRTHPSATVHNPTRIKLMK 172
DB 148 GSYSSVSIQVANNLLRFQIPQISYASTSAKLSKSDYFARTVPPDFYQAKAMAILRF 207
QY 173 FQWSRVAILQAAEEVFISTVEDE-----NRCMEAGVEIVTRQSFSLSDPTDAVRN-LRR 225
DB 208 FMTVSTVTSVASEGDYGTGIEAFEQEARLNICI-ATAEKVGRSNIRKSYDSVIRELLQK 266
QY 226 QDARIIVGLFYVVAARRVLCENYKQOLYGRAHWFFIGWY-EDNW--YEVNLKAE----- 277
DB 267 PNARVVVLMRSDDSRELIATAA-----SRANASF--TWVADGWAQESIIKGSHEVAY 318
QY 278 -GITCTVEQMRIAAGHILTTEALMNQNNQTTISGMTAEFR-----HRLNQALIEEGYD 331
DB 319 GDITLELASQPVRFQGRYFQSLNPNYNNHRNPWFDRFWEQKFCQSLQNKRRHVRVCEKHLA 378

Qy 332 INHDYPEGYOEAPLAY--DAVWSVALAFNKTWERL---TT-----GKKSURDF- 375
Db 379 IDSSNYE---QESKIMFVNNAVYAMAHALKMORTLCPNPTTKLCDAMKILDGKKLYKDYL 435
Qy 376 -----TYTDKEIADEI-----YAAMNSTOFLGVGVVAFSSQG----- 408
Db 436 LKINFTAFPNPKDADSIVKFDFTGDMGRYVNFQNVGGKYSYLVKVGHWAEITSLDVN 495
Qy 409 -----DRIALTQIEQMIDG-----KYEKL----- 427
Db 496 SIHWSRNSVPTSQSDPCAPNEMKNMOPGDVCCWICIPCPEYELADEFTCMDCSGGQWP 555
Qy 428 -----GYDQTOLDNLWNLTEQWIGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFV 482
Db 556 TADLTGCDLPEDYIRW--EDAWAIGPV-----TIACLGFMCTC----- 592
Qy 483 AFALIFINWKNHRR---VIOSSHVPNCNTIMLFGVIICLISVILLGIDGRFVSPEEYPKI 539
Db 593 ---MVTVFIKHNTPLVKASGRELC-YILLFGVGLSYCMTF-----FFIAKPSVI 640
Qy 540 COARAWLLSTGFTLAYGAMFSKVRVHRTTAKTDPK--KKVEPWKLYTMVSGLLSIDL 597
Db 641 CALRRLGLGSSFAICYSALLTKTNCIARIFDGVKNGAQRPKFISPSQVFCIGLILVQI 700
Qy 598 VILLSWOIFDP--LQRYL-----ETFPLEDVSTDDIKIRPELEHCEQSRNSMWGLVY 650
Db 701 VMVSWMLILEAPGTRRYTLAERETVILK-----CNVKDSMLISLT 743
Qy 651 GFKGLILVFLGLAYETRSIKVKQINDSRVGMISYVNVVLCITAPVGMVIAQQODASF 710
Db 744 DV--ILVILCTVYAFKTRKCP-ENFNEAKFIFTMTTCIIWLAFILPIFYVTSDDYRVQT 800
Qy 711 AFVALAVIFCCFLSMILLIFVPKVIEWIRHPK 741
Db 801 TTMCSISVLSGFVILGCLFAPKPVHILFQPQ 831
RESULT 15
US-08-486-270-6
; Sequence 6, Application US/08486270
; Patent No. 5807689
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen
; APPLICANT: Pontsler, Aaron
; APPLICANT: Johnson, Edwin C.
; APPLICANT: Hess, Stephen D.
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
; NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,270
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/072,574
; FILING DATE: 04-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: FP41 9772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 879 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-270-6
Query Match 7.5%; Score 328; DB 1; Length 879;
Best Local Similarity 20.1%; Pred. No. 5.5e-24;
Matches 175; Conservative 134; Mismatches 320; Indels 242; Gaps 36;
Qy 36 ELHTGGIEPTAGGMOGQAC-----MPATRLALDDVKNOPNLPLGPKLILHS 84
Db 38 DLVLGGGLFPINKEG--TGTEECGRINEDRGIORLEAMLFADIDEINKDODYLLPGVKLVGHI 95
Qy 85 NDS-----ECEPGLGASVMYNNLYNKPQKMLLAGC-- 115
Db 96 LDTCSRDTYALEOSLEFVRASLTWKVDEAYMCPDG-----SYAQENIP---LLIAGVIG 147
Qy 116 ---STVCTTVAEAAKMMNLLVLCYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKMKK 172
Db 148 GSYSSVSIQVANLLRLFIQISYASTSAKLSKRSRYDFARTVPPDFYQAKAMAEILRF 207
Qy 173 FGSRVAILQOAEVFISTVEDLE-----NRCMEAGVEIVTROSFLSDPTDAVRN-LRR 225
Db 208 FNTYTVTVASEGDIYGETIEAFQEAEARLNICI-ATAEKVGRSNIRKSYDSVIRELLQK 266
Qy 226 QDARIIVGLFVVAARRVLCEMYKQOLYGRAHVWFFIGWY-EDNW--YEVLKAE----- 277
Db 267 PNARVVVLFWRSDSRELIAA-----SRANASF--TWASDGGWQAEIISKSEHWAY 318
Qy 278 -GITCTVEQMRIAEEHGLTTEALMNNONOTTISGMTAEFR-----HRLNOALIEBGD 331
Db 319 GDITLELASQPVRFGRYFQSLNPNYNNHNPWFDFWEQKFOCSLQNRNRRVCEKHLA 378
Qy 332 INHDYPEGYOEAPLAY--DAVWSVALAFNKTWERL---TT-----GKKSURDF- 375
Db 379 IDSSNYE---QESKIMFVNNAVYAMAHALKMORTLCPNPTTKLCDAMKILDGKKLYKDYL 435
Qy 376 -----TYTDKEIADEI-----YAAMNSTOFLGVGVVAFSSQG----- 408
Db 436 LKINFTAFPNPKDADSIVKFDFTGDMGRYVNFQNVGGKYSYLVKVGHWAEITSLDVN 495
Qy 409 -----DRIALTQIEQMIDG-----KYEKL----- 427
Db 496 SIHWSRNSVPTSQSDPCAPNEMKNMOPGDVCCWICIPCPEYELADEFTCMDCSGGQWP 555
Qy 428 -----GYDQTOLDNLWNLTEQWIGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFV 482
Db 556 TADLTGCDLPEDYIRW--EDAWAIGPV-----TIACLGFMCTC----- 592
Qy 483 AFALIFINWKNHRR---VIOSSHVPNCNTIMLFGVIICLISVILLGIDGRFVSPEEYPKI 539
Db 593 ---MVTVFIKHNTPLVKASGRELC-YILLFGVGLSYCMTF-----FFIAKPSVI 640
Qy 540 COARAWLLSTGFTLAYGAMFSKVRVHRTTAKTDPK--KKVEPWKLYTMVSGLLSIDL 597
Db 641 CALRRLGLGSSFAICYSALLTKTNCIARIFDGVKNGAQRPKFISPSQVFCIGLILVQI 700
Qy 598 VILLSWOIFDP--LQRYL-----ETFPLEDVSTDDIKIRPELEHCEQSRNSMWGLVY 650
Db 701 VMVSWMLILEAPGTRRYTLAERETVILK-----CNVKDSMLISLT 743
Qy 651 GFKGLILVFLGLAYETRSIKVKQINDSRVGMISYVNVVLCITAPVGMVIAQQODASF 710
Db 744 DV--ILVILCTVYAFKTRKCP-ENFNEAKFIFTMTTCIIWLAFILPIFYVTSDDYRVQT 800

QY 711 AFVALAVIFCCFELSMILLIFVPKVIEWIRHPK 741
Db 801 TTMCISSVLSGFEVVLGCLFAPKVHILLFPQ 831

Search completed: April 30, 2002, 10:12:32
Job time: 209 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:10:58 ; Search time 27.28 Seconds
(without alignments)
2280.849 Million cell updates/sec

Title: US-09-715-962-2

Perfect score: 4374

Sequence: 1 MKRDMTSGAVTFWIFLLCL.....LINSASHTAATPAATLAIQTGE 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	4374	100.0	840	22	AAB86159 D. melanogaster GA
2	2035	46.5	844	19	AAW40119 Human GABA-BR1b re
3	2035	46.5	844	20	AAW40119 Human GABA-BR1b re
4	2035	46.5	844	20	AAW40119 Human GABA-BR1b re
5	2035	46.5	844	21	AAW40119 Human GABA-BR1b re
6	2034.5	46.5	844	21	AAW40119 Human GABA-BR1b re
7	2032	46.5	844	19	AAW40119 Human GABA-BR1b re
8	2031.5	46.4	964	20	AAW40119 Human GABA-BR1b re
9	2030.5	46.4	960	21	AAW40119 Human GABA-BR1b re
10	2030.5	46.4	961	20	AAW40119 Human GABA-BR1b re
11	2030.5	46.4	961	20	AAW40119 Human GABA-BR1b re

12	2030.5	46.4	961	20	AAW40119 Human GABA-BR1b re
13	2030.5	46.4	1323	20	AAW40119 Human GABA-BR1b re
14	2029.5	46.4	793	19	AAW40119 Human GABA-BR1b re
15	2029.5	46.4	892	20	AAW40119 Human GABA-BR1b re
16	2029.5	46.4	960	19	AAW40119 Human GABA-BR1b re
17	2029.5	46.4	962	22	AAW40119 Human GABA-BR1b re
18	2028.5	46.4	960	20	AAW40119 Human GABA-BR1b re
19	2026	46.3	844	20	AAW40119 Human GABA-BR1b re
20	2026	46.3	844	20	AAW40119 Human GABA-BR1b re
21	2023.5	46.3	960	20	AAW40119 Human GABA-BR1b re
22	2023.5	46.3	960	20	AAW40119 Human GABA-BR1b re
23	2023.5	46.3	960	22	AAW40119 Human GABA-BR1b re
24	1967	45.0	886	22	AAW40119 Human GABA-BR1b re
25	1721	39.3	753	22	AAW40119 Human GABA-BR1b re
26	1290	29.5	941	21	AAW40119 Human GABA-BR1b re
27	1290	29.5	941	21	AAW40119 Human GABA-BR1b re
28	1290	29.5	941	21	AAW40119 Human GABA-BR1b re
29	1290	29.5	941	21	AAW40119 Human GABA-BR1b re
30	1290	29.5	941	21	AAW40119 Human GABA-BR1b re
31	1290	29.5	941	21	AAW40119 Human GABA-BR1b re
32	1290	29.5	941	22	AAW40119 Human GABA-BR1b re
33	1290	29.5	943	20	AAW40119 Human GABA-BR1b re
34	1289	29.5	941	21	AAW40119 Human GABA-BR1b re
35	1287	29.4	940	21	AAW40119 Human GABA-BR1b re
36	1285.5	29.4	914	21	AAW40119 Human GABA-BR1b re
37	1285.5	29.4	965	21	AAW40119 Human GABA-BR1b re
38	1285	29.4	1303	20	AAW40119 Human GABA-BR1b re
39	1284	29.4	898	20	AAW40119 Human GABA-BR1b re
40	1284	29.4	898	21	AAW40119 Human GABA-BR1b re
41	1283	29.3	940	21	AAW40119 Human GABA-BR1b re
42	1283	29.3	940	21	AAW40119 Human GABA-BR1b re
43	1282	29.3	940	21	AAW40119 Human GABA-BR1b re
44	1263	28.9	883	20	AAW40119 Human GABA-BR1b re
45	1249.5	28.6	473	20	AAW40119 Human GABA-BR1b re

ALIGNMENTS

RESULT 1

AAB86159 ID AAB86159 standard; Protein; 840 AA.

XX AC AAB86159;

XX DT 03-AUG-2001 (first entry)

XX DE D. melanogaster GABA-B receptor protein SEQ ID 2.

XX KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
XX KW insecticide/transgenic invertebrate; plant protection agent;
XX KW human medicine; veterinary medicine; insect.

XX OS Drosophila melanogaster.

XX PN DE19955408-A1.

XX PD 23-MAY-2001.

XX PF 18-NOV-1999; 99DE-1055408.

XX PR 18-NOV-1999; 99DE-1055408.

XX PA (FARB) BAYER AG.

XX PI Raming K, Mezler M, Mueller T;

XX DR WPI; 2001-318282/34.

XX DR N-PSDB; AAH20519.

XX PT New invertebrate gamma-aminobutyric acid receptor proteins, useful in screening for potential insecticides, for plant protection or medicine, also related nucleic acid

XX PS Claim 2; Page 16-21; 62pp; German.

XX CC This invention describes a novel polypeptide (I), functioning as a

CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal

CC activity. (I), also the nucleic acid (II) that encodes it and related

CC vectors, host cells, antibodies and transgenic invertebrates, are used

CC for identifying: (i) new plant protection agents, i.e. modulators of (I)

CC with insecticidal activity, which may also be useful in human or

CC veterinary medicine; and (ii) genes that encode polypeptides involved in

CC assembly of functionally related GABA-B receptors in insects. This

CC sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor

CC which is described in the method of the invention.

XX XX Sequence 840 AA;

Query Match 100.0%; Score 4374; DB 22; Length 840;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRKDMTSDGAVTFWIFLCLLIASPHLQGGVAGRPDELHIGGIFPIAGKGGWQGGACMPA 60

DB 1 mrkdmtsdgavtfwiflclliasp hlggvgagrpdelhiggi fpiagkgggwggacmpa 60

QY 61 TRALDDVNKQPNLLPGFKLIHSNDSCEPGLGASVWYNLLNKPOKMLLAGCSTVCT 120

DB 61 tralddvnkqpnllpgfklihsndsecepglgasvymynllnkpokml laggcstvct 120

QY 121 TVAAAKMNLIVLCYGASSPALSDDRPPTLFTHPSAVHNPTRIKLMKKFCWSVAI 180

DB 121 tvaaakmnlivlcygasspalsdrk rptlfrthpsatvhnptrikl mkkfgwsval 180

QY 181 LQAAEFVISTVEDLENRCMEAGVEIVTRQSFSLSDPTDAVNRRLRRQDARIIVGLFYVAA 240

DB 181 lqaaefvistvedlenrcmeagveivtrqsfslsdptdavnrrlrrqdariivglfyvaa 240

QY 241 RRVLCMEYKQOLYGRHVVFFIGWYEDNMYEVNKLKAGITCTVEQMFIAEGHLLTTEALM 300

DB 241 rrvlcemykqlygrhvvffigwyednmyevnklkagitctveqmfiaeghl lttealm 300

QY 301 WNONNOTTISGMTAEFRHLNQAALFEGVDINHDPYEGYQEAFLAYDAVSWALAFNK 360

DB 301 wnonnottisgmtaefrhl nqaalfegvdi nhdrypegyqeaflayd avswalafnk 360

QY 361 THERLTGKSLRDFYTTDKIEADEIYAAMNSTQFLGVSQVAFSSQGDRIALTQIQEMI 420

DB 361 tmerltgkslrdfytt dkieadeiyaamn stqflgvsqvafssqgdrialtqieqmi 420

QY 421 DGKYEKLYYDTOLDNLWSLNTQEWIGGKVPQDRTIVTHVLRVSLPLFCVCMPISSCGI 480

DB 421 dgkyeklyydtoldn lswlnteqwigkv pqpdrti vthvlsrplfvc mctisscgi 480

QY 481 FVAFALTIENWKNHRRVIOSSHPVCNTIMLFGVILCLISVILLIGIDGRFVSPEEYKIC 540

DB 481 fvafalti enwknhrv ioss hvpvcntiml fgvilclisvillig idgrfvspeeykic 540

QY 541 QARAWLLSTGFTLAYGAMFQKVRVHRTTKAKTDPKKKPEWPKLYTMWSGLLSIDILVIL 600

DB 541 qarawllstgftlay gamfqr vhrfttkaktdpkkpewklytmwsgllsidilvil 600

QY 601 LSWQIFDPLQRYLETFFPLEDPVSTDDIKIRPELEHCEQSNMWSLGLVYGFKGLIILVFG 660

DB 601 lswqifdplqrylet fpledpvstddik irpelehesqsnmws lglvygfgkllilvfg 660

QY 661 LFLAYTRSIVKQINDSRVGSINVVVLCITAPVGMVIAQQDASFAFVALAVIFC 720

DB 661 lflaytrsivkqindsr vgsinvvv lclitapvgmviasqqdasfafvalavifc 720

QY 721 CFISSLMLLIFVPKVIEWIRHPKDKAESKYNPDPSAISKEDEERYQKLVNTENQOLRLITQKE 780

DB 721 cfissml lifvpkviewir hpkdkaeskynp dpsaisked eeryqklvnt enqolrlitqke 780

QY 781 EKIRVLQRILVERGDAGKTELGATGVASAAVATTSPASLINSASAHATPAATLAIQTGE 840

DB 781 ekirvlqrilvergdagk teingatgvasaavattspas linsasahatpaatla itqge 840

RESULT 2

AAW40119

ID AAW40119 standard; Protein; 844 AA.

XX AC AAW40119;

XX DT 03-JUN-1998 (first entry)

XX DE Human GABA-BR1b receptor protein.

XX KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;

KW inhibitory neurotransmitter; peripheral nervous system; antagonist;

KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;

KW epilepsy; cognitive function.

XX OS Homo sapiens.

XX PN WO9746675-A1.

XX PD 11-DEC-1997.

XX PF 19-MAR-1997; 97WO-EP01370.

XX PR 22-NOV-1996; 96US-0756091.

XX PR 30-MAY-1996; 96US-0655716.

XX PA (NOVS) NOVARTIS AG.

XX PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;

XX WPI: 1998-042183/04.

XX DR N-PSDB; AAV10267.

XX PT Purified GABA-B receptor or receptor protein - and antagonists of

PT these which may be useful in treating nervous system disorders

XX Claim 4; Page 86-90; 108pp; English.

CC This sequence represents a novel human GABA-B receptor protein,

CC GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory

CC neurotransmitter found in the brain and peripheral nervous system

CC and this receptor may be used for the identification of GABA-B

CC receptor agonists and antagonists. Such proteins may be used in

CC treatment of dementia, depression, anxiety, epilepsy, spasticity,

CC bronchial inflammation or asthma or to improve cognitive function.

CC GABA-B receptor ligands and probes derived from this sequence can be

CC used to assay for GABA-B receptors or DNA encoding them.

XX SQ Sequence 844 AA;

Query Match 46.5%; Score 2035; DB 19; Length 844;

Best Local Similarity 49.3%; Pred. No. 7.5e-193;

Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;

QY 23 SPHL---QGVAGRDE----LHIGGIFPIAGKGGWQGGACMPATRIALDDVNKPNLL 75

DB 23 sphlprphsrpvp hpserrav yigalfpms--ggwp gggqacq pavema ledvnsrrdl 89

QY 76 PGFKLIHSNDSCEPGLGASVWYNLLNKPOKMLLAGCSTVCTVTAEAAMNLLIVLC 135

DB 76 pgyelk lihsdskdpggatk ylyell yndpik ilmpgcssvstlv aeaamnlivls 149

QY 136 YGASSPALSDDRPPTLFTHPSAVHNPTRIKLMKKFCWSRVAILQAAEFVISTVEDL 195

DB 136 ygsaspalsnrrq rftfrthpsatv hnptrk lmkfkfwgk kiatqgttevtltdl 209

QY 196 ENRCMEAGVEIVTRQSFSLSDPTDAVNRRLRRQDARIIVGLFYVAAARRVLCMEYKQOLYGR 255

Db 210 eervkeagieitfrdfssdpavpknkrqdarlivglfyetearkvfveykerlfgk 269
 Qy 256 AHVFFIGWYEDNMYEVLKAEIGITVEQMRIAEGHLTTEALMWNQNNQTTISGMTAE 315
 Db 270 kyvfwligyadnwfk--ydpinctvdmteaveghitteivmlnpantrsismntsq 327
 Qy 316 EFRHRLNQAALIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNPKTMRLETGKKSL 372
 Db 328 efvekitkrl-----krhpeetggfqaepalaydaialalalnktsgggrsgvrl 378
 Qy 373 RDTYTDKEIADEIYAAMNSTQFLGVSVAFSSQGDRIALTOIEQMIDKYEKLGYDT 432
 Db 379 edfnynqntitdqiyrannsssfegshvfdasgrmawtlieqlggsgykkigyds 438
 Qy 433 QLDNLWLNTAEQWIGKVPQDRITVHVLTSLPLFVCMCTISSCGIFVAFALIFNIW 492
 Db 439 tkddlswektkwiggspadqtlviktfrflsqklfsvslsagvlavvcslfnly 498
 Qy 493 NKHRRVIOSSHVPVCNTIMLFGVIICLSIVLLGIDGRFVSPPEYPKICQARAWLLSTGFT 552
 Db 499 nshvryiqnsqpnlnltavgsclalaavfplgldgynhgrnqfpfvcqarlwlglgfs 558
 Qy 553 LAYGAMFSKVRVHRFTTK--AKTDPKKKVEPWKLYTWVSGLLSIDLVLLSQIFDPDQ 610
 Db 559 lgygsmftkiiwwhtvftkkekewrktlepklyatvgllvgmdivltaiwqivdplh 618
 Qy 611 RYLETFFLEDVSTDDIKIRPELECHESQORNWGLVYGFGLIILVFLGFLAYETRSI 670
 Db 619 rtietfakeepkedi-dvslilpqlchcscrkmtwtgfygkglillgflayetkvs 677
 Qy 671 KVKQINDSRVGMSTYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLI 730
 Db 678 stekindhvragmalyavclitcapvtmllssqdaafafaslaivfssyitlvvlfv 737
 Qy 731 PKVIEVIRHP--KKAESKYNPDSAISKEDERYQKLVTEENQQLRLITQKEEKIRVL 788
 Db 738 pkmrllitrgewqseqdmtkgsstnnneeksrlllekenrelekiiaekervselrh 797
 Qy 789 RLVER 793
 Db 798 qlqsr 802

RESULT 3
 AAY28839
 ID AAY28839 standard; Protein: 844 AA.
 XX
 XX AAY28839;
 XX 17-JAN-2000 (first entry)
 XX Human GABABR1b receptor protein.
 XX GABABR1b receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
 KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
 KW synaptic transmission; GABABR1b; cloned receptor; splice variant;
 KW modulatory agent; molecular activity assay; antispastic; anti-addictive;
 KW antineurodegeneration; analgesic; cardiovascular activity.
 XX
 OS Homo sapiens.
 XX
 XX WO9951636-A2.
 XX
 XX 14-OCT-1999.
 XX
 XX 02-APR-1999; 99WO-US07352.
 XX
 XX 03-APR-1998; 98US-0080676.
 XX
 XX (NPS-) NPS PHARM INC.
 XX
 XX Garrett JE, Simin RT, Busby JG, Stormann TM;

XX WPI; 1999-610994/52.
 DR N-PSDB; AAX90921.
 XX
 PT Novel nucleic acids, used to screen for specific modulators, e.g. for
 PT treating spasticity or Alzheimer's disease
 XX
 PS Disclosure; Fig 2A-2E; 78pp; English.
 XX
 XX The present sequence encodes GABABR1b receptor protein cloned from rat
 CC brain. This is closely related to GABABR2. GABAB receptors are
 CC metabotropic receptors that modulate synaptic transmission in brain.
 CC GABABR1a differs from GABABR1b in that the N-terminal 147 residues are
 CC replaced by 18 amino acids. Both of these cloned receptors appear to be
 CC splice variants. They are expressed in cells that express GABABR2. This
 CC nucleotide sequence is used to screen for specific modulators. These
 CC modulators have antispastic, antineurodegeneration, analgesic, anti
 CC -addictive, cardiovascular activities.
 CC Note: SEQ ID NO. 8 is referred as the GABABR1a receptor protein in
 CC the specification.
 XX
 SQ Sequence 844 AA;
 Query Match 46.5%; Score 2035; DB 20; Length 844;
 Best Local Similarity 49.3%; Pred. No. 7.5e-193;
 Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
 Qy 23 SPHL---QGVVACRPDE---LHIGGFPTAGKGGGQACMPATRLALDDVKNQNL 75
 Db 32 sphlprphsvrpphserravyigalpfms--ggvpggacqavemaiedvnrsrdil 89
 Qy 76 PGFKLILHNSDCEPCGLGASVMNLLYKPKMLLAGCTVCTTVAEAKMNLVLC 135
 Db 90 pdyellihndskcdp9gatklyellyndpikiilmpgcvsvstlvaearmnllivs 149
 Qy 136 YGASSPALSDRKRPFTLFRTHPSATVHNPTRIKMKFGWSRVAILQAQAEVFTSTVEDL 195
 Db 150 ygsspalnsnqrpftrfthpsatilhnptrvklfkgwkkkiatqtevtftstid 209
 Qy 196 ENRCMAGVEIVTRQSFSLDPTDAVNLRRQDARIIVGLFVYVAARRVLCMKYQYGR 255
 Db 210 eervkeagieitfrsfssdpavpknkrqdarlivglfyetearkvfveykerlfgk 269
 Qy 256 AHVFFIGWYEDNMYEVLKAEIGITVEQMRIAEGHLTTEALMWNQNNQTTISGMTAE 315
 Db 270 kyvfwligyadnwfk--ydpinctvdmteaveghitteivmlnpantrsismntsq 327
 Qy 316 EFRHRLNQAALIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNPKTMRLETGKKSL 372
 Db 328 efvekitkrl-----krhpeetggfqaepalaydaialalalnktsgggrsgvrl 378
 Qy 373 RDTYTDKEIADEIYAAMNSTQFLGVSVAFSSQGDRIALTOIEQMIDKYEKLGYDT 432
 Db 379 edfnynqntitdqiyrannsssfegshvfdasgrmawtlieqlggsgykkigyds 438
 Qy 433 QLDNLWLNTAEQWIGKVPQDRITVHVLTSLPLFVCMCTISSCGIFVAFALIFNIW 492
 Db 439 tkddlswektkwiggspadqtlviktfrflsqklfsvslsagvlavvcslfnly 498
 Qy 493 NKHRRVIOSSHVPVCNTIMLFGVIICLSIVLLGIDGRFVSPPEYPKICQARAWLLSTGFT 552
 Db 499 nshvryiqnsqpnlnltavgsclalaavfplgldgynhgrnqfpfvcqarlwlglgfs 558
 Qy 553 LAYGAMFSKVRVHRFTTK--AKTDPKKKVEPWKLYTWVSGLLSIDLVLLSQIFDPDQ 610
 Db 559 lgygsmftkiiwwhtvftkkekewrktlepklyatvgllvgmdivltaiwqivdplh 618
 Qy 611 RYLETFFLEDVSTDDIKIRPELECHESQORNWGLVYGFGLIILVFLGFLAYETRSI 670
 Db 619 rtietfakeepkedi-dvslilpqlchcscrkmtwtgfygkglillgflayetkvs 677
 Qy 671 KVKQINDSRVGMSTYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLI 730

Db 678 steindhravgmalynavvclitapvmtlssqdaafafaslaivfssytlvlfv 737
QY 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDERYQKLVTEQOLRLITQKEKIRVLRQ 788
Db 738 pkmrllitrgewqseaqdmktgsstnnneeksrillekenrelekiaaekeervselrh 797
QY 789 RLVER 793
Db 798 qlqsr 802
RESULT 4
RAY14102
ID AAY14102 standard; Protein; 844 AA.
XX
AC AAY14102;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor 1b protein sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.
XX
OS Homo sapiens.
XX
PN W09921890-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98WO-SE01947.
XX
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
PA (ASTR) ASTRA AB.
XX
PI Ekstrand J;
XX
DR WPI; 1999-302985/25.
DR N-PSDB; AAX58055.
XX
PT Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX
PS Claim 17; Page 90-94; 222pp; English.
XX
CC This sequence is a human gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB Ric or 1b,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.
XX
SQ Sequence 844 AA;
Query Match 46.5%; Score 2035; DB 20; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
QY 23 SPHL---QGVAGRPE---LHIGIFPIAGKGGMOGQACMPATRLALDDVKNQPNLL 75

Db 32 sphlprhpsrvppsserravyigalfpms--ggwpggacqcpavemaledvnsrrdil 89
QY 76 PGFKLIHSDNSECEPGLGASQVWYNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIIVLC 135
Db 90 pdyelkiihdsckdpggatkyllyllyndpikilmpgcssvstlvaeaaarmnllvls 149
QY 136 YGASSPALSDRKREPTLFRHPSATVHNPTRIKLMKFKGSRVAILQQAAEEVFISTVEDL 195
Db 150 ygasspalsnrqrfptfrthpsatlhnptrvki fexgwkkiaitqgttevtstlddl 209
QY 196 ENRCMEAGVEIVTROSFLSDPTDAVRNLRODAIIIVGLFVVAARRVLCSEMYKQOLYGR 255
Db 210 eervkeagieltfrqsfssdpavpvknkrqdarilvlgfyetearkvfcevyeerlfgk 269
QY 256 AHVFFFGWYEDNMYEYNLKAEGTCTVEQMRIAEGLHTEALMWNONNONTTSGMFAE 315
Db 270 kyvfwlligwyadnwfk1--ydpssinctvdemteaveghitteivmlpantrsisnmtsq 327
QY 316 EFRRLNQALIEEGYDINHRYPE---GYQEAPLAYDAVWSVALAFNKTMERLTGKKSL 372
Db 328 efvekltkrl-----krhpeetgfgqaplaydaivalalalnktsgggrsgvrl 378
QY 373 RDEYTKETADEIYAAAMNSQFGLVSGWAFSSQGDRIALTOIEMIDGKYEKLYYDT 432
Db 379 edfynnqtlcdqlyramsssfegvshvfdasgsrmatlleqigggyskkygyyds 438
QY 433 QLDNLWLNTQWIGGKVPQDRTIVTHVLRVSLPLFCMCTISSCGIFVAFALIFNIW 492
Db 439 tkddlsksktdkwiggspadqtlviktfrfslqklfsvslsglavlavvcslsfny 498
QY 493 NKRRVQTOSHPVONTIMLFVITCLISVILLGDGRVSPPEEPKICQARAWLLSTGFT 552
Db 499 nshvryiqnsqpnlnltavgcslalaavfplgidyghgrnqpfvcoqarlwlilglfs 558
QY 553 LAYGAMFSKYWRVHRFTK--AKTDPKKKVPKLYTMVSGLSLTDLVLLSQWDFDPLQ 610
Db 559 lgygsmftkiwwhtvftckeeekewrktlepwklyatvgllvmdvltlaivqldplh 618
QY 611 RYLETFPLEDPVSTDDIKIRPELEHESQNSMWMGLVYGFGLVFLGFLAYETRSI 670
Db 619 rtietfakkepke di-dvsilpqiehcscrkmtwlgfygkglillilgflayetksv 677
QY 671 KVKQINDSRVYGMSTIYNVVVLCLITAPVGMVIAQQDASAFVALAVITCCFLSMLLIFV 730
Db 678 stekindhvragmalynavvclitapvmtlssqdaafafaslaivfssytlvlfv 737
QY 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDERYQKLVTEQOLRLITQKEKIRVLRQ 788
Db 738 pkmrllitrgewqseaqdmktgsstnnneeksrillekenrelekiaaekeervselrh 797
QY 789 RLVER 793
Db 798 qlqsr 802
RESULT 5
AAY32467
ID AAY32467 standard; Protein; 844 AA.
XX
AC AAY32467;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human G-protein coupled receptor GABAB1b.
XX
KW GABAB1b; G-protein coupled receptor; human; antibacterial;
KW antiviral; virucide; antiparasitic; analgesic; cytostatic;
KW antidiabetic; anorectic; cardiant; antiparkinsonian;
KW hypertensive; hypotensive; antiemetic; osteopathic; antianal;
KW cerebroprotective; antitumor; antiallergic; neuroleptic;
KW tranquilizer; antidepressant; nootropic; antimitragine;
KW anticonvulsant; neuroleptic; agonist; antagonist; inhibitor;


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QY 191 TVELENRCMEAGVEIVTRQSFSLSDPTDAVRNLRQDARIIVGLFVVAARRVILCEMYKO 250
Db 192 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 205 tldleervkeagieitfrfsfpavpvknkrqdarivglfyetearkvfevyke 264
Db 206 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 251 QLYGRAHVWFPIGWEDNWNVNLKAGITCTVEQMTAAEGHLEALTEALMWNQNTTIS 310
Db 252 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 265 rlfqkkyvffligyadnwft--ydpnsinctveemteavegnitvmlpantrris 322
Db 266 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 311 GMTAEFRHRLNQLIEBGIYDINHRYPE--GYOEAPLAYDAVMSVALAFNKTMERLTT 367
Db 312 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 323 nmtsgefvekitkrl-----krhpeetggfcpaydaialalalanktsgggr 373
Db 324 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 368 GKSLRDPYTDKEIADIYAMNSTQFLGVSGVVAFFSQGDRIALTOIEQMDIKYEKL 427
Db 369 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 374 sgvrledfnynqittdqiyramsssfegvghvfvfdaasgrmawtlieqiggyykki 433
Db 375 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 428 GYDTQDLNLSWLNTEQWIGKVPQDRTIVHVLRTVSLPLFVCMCTISSCGIFVAFALI 487
Db 429 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 434 gyydstkdlswsktdkwiggspadqtlvktfrlsgklfsvsvissigivlavcl 493
Db 435 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 488 IFNIWNKHRRYIQSHPCNTIMLFGVILICLISVILLGIDGRFVSPPEVPKICQARALL 547
Db 489 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 494 sfniynshvriqspnlmltavgcsalaaavfplgdghygrsqfpvcqarlwl 553
Db 495 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 548 STGFTLAYGAMFSKVRVHREFTK--AKTDPKKKVEPWKLXTMWSGLSIDLVILLSWQI 605
Db 549 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 554 glgfslygsmftkiwwhtvftkkekewrktlepkwkyatvgllvgmdvltaiwqi 613
Db 555 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 606 FDPQRYLETFPLEDPVSTDDIKRPELHCESSORNSMGLVGLVFGKLILVFLGLAY 665
Db 607 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 614 vplhrtietfakeepedi--dvsilpqlehcckmtwigfygkglllilgliflay 672
Db 615 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 666 ETRSIKVKQINDSRVGMISYNNVVLCLITAPGVNVIASQODASAFVALAVIFCCFLSM 725
Db 667 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 673 etkvsstekindhavgmaiynavclitapvtmllssqqdaafafaslaivfssyti 732
Db 674 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 726 LLIFVPKVIEWIRHPKKAESK--YNPDSAISKEDEERYQKLVTEQOLRLITOKEEKI 783
Db 727 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 733 vvlfpkmrlitrgewqsetqdtmktgssnnneeksrillekenrelekiiaekeerv 792
Db 734 :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 784 RVLQRIVER 793
Db 793 selrhqlqsr 802

RESULT 8
ID AAY14105
AC AAY14105 standard; Protein; 964 AA.
XX AAY14105;
XX AAY14105;
XX 21-JUL-1999 (first entry)
XX Canine GABAB receptor la protein sequence.
DE Canine GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
XX autoimmune disease; neoplastic disease; infectious disease; therapy.
XX Canis familiaris.
XX Canis familiaris.
XX W09921890-A1.
XX 06-MAY-1999.
XX 27-OCT-1998; 98WO-SE01947.
XX 17-JUL-1998; 98SE-0002575.
XX 27-OCT-1997; 97SE-0003914.
XX 16-MAR-1998; 98SE-0000864.

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XX

(ASTR) ASTRA AB.

PA

Ekstrand J;

XX

WPI: 1999-302985/25.

DR

N-PSDB; AAX58058.

XX

Polynucleotides encoding human and canine gamma aminobutyric acid type B receptors, used to screen for compounds that are inhibitors of transient lower oesophageal sphincter relaxations

PT

Claim 17; Page 99-105; 222pp; English.

PS

XX

This sequence is a canine gamma aminobutyric acid type B (GABAB) receptor of the invention. Nucleic acid molecules encoding GABAB receptors can be used to screen for compounds that are inhibitors of transient lower oesophageal sphincter relaxations (TLESR). They can also be used to screen for agonists or antagonists of the GABAB receptors. Inhibitors of TLESR are useful for treating gastro-oesophageal reflux disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d, comprise diagnosis or treatment of conditions related to GABAB dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune diseases, neoplastic diseases, pain and infectious disease.

Sequence 964 AA;

SQ

Query Match 46.4%; Score 2031.5; DB 20; Length 964;

Best Local Similarity 49.4%; Pred. No. 2.1e-192;

Matches 386; Conservative 152; Mismatches 216; Indels 27; Gaps 9;

QY 24 PHLOGVAGRPDE----LHIGGFIPTAGKGGWGGGACMPATRLADDVKNQNLPGFK 79

Db 158 phqc--vstrphserravvigaifpms--ggwpggacpavemaiedvnsrrdiipdye 213

QY 80 LILHSDSECEPLGASVMVNLKPKOKMLLAGSGSTVCTTVAEAKMNLVLCVGAS 139

Db 214 klhhdskcdpqqatkyellyndpikilmpgcsstvlvaearmnllvlsygs 273

QY 140 SPALSDRKRPFTLFRTHPSATVHNPTRIKLMKFGSRVAILQOAEVFTSTVEDLENRC 199

Db 274 spalsnrqfptfrthpsatlnhptrvklfekwgrkatiqgttevfstiddeerv 333

QY 200 MEAGVEIVTRQSFSLSDPTDAVRNLRQDARIIVGLFVVAARRVILCEMYKQLYGRAHVW 259

Db 334 keagieitfrfsfpavpvknkrqdarivglfyetearkvfevykerifgkkyv 393

QY 260 EFIGWYEDNWNVNLKAGITCTVEQMTAAEGHLEALTEALMWNQNTTISGMTAEFRH 319

Db 394 fligwyadnwft--ydpnsinctvdeemteavegnitvmlpantrrisnmtsgefe 451

QY 320 RLNQLALIEBGIYDINHRYPE--GYOEAPLAYDAVMSVALAFNKTMERLTTGKSLRDFT 376

Db 452 kitkrl-----krhpeetggfcpaydaialalalanktsggsgsrgrvledfn 502

QY 377 YTDKEIADIYAMNSTQFLGVSGVVAFFSQGDRIALTOIEQMDIKYEKLGYDYFDOLDN 436

Db 503 ynnqittdqiyramsssfegvghvfvfdaasgrmawtlieqiggyykkiyydstkdd 562

QY 437 LSWLNTEQWIGKVPQDRTIVHVLRTVSLPLFVCMCTISSCGIFVAFALIFINIKNHR 496

Db 563 lswsktdkwiggspadqtlvktfrfmsqklfsvsvissigivlavclsnfynshv 632

QY 497 RVIOSSHPCNTIMLFGVILICLISVILLGIDGRFVSPPEVPKICQARALLSFGFTLAYG 556

Db 623 ryiqnsqpnmltavgcsalaaavfplgdghygrsqfpvcqarlwlilglfslggy 682

QY 557 AMFSKVRVHREFTK--AKTDPKKKVEPWKLXTMWSGLSIDLVILLSQIFDPLQRYLE 614

Db 683 smftkiwwhtvftkkekewrktlepkwkyatvgllvgmdvltaiwgmvdplhrtie 742

QY 615 TPLEDPVSTDDIKIRPELHESORNSMWGLVYGFKGLIIVFLGFLAYETRSIKVKQ 674
 Db 743 tfakeepedi-dvslpqhccsskmmwtgifygkglililgflayetskystek 801
 QY 675 INDSRYVGSINVVVLCITAPVGVVIASQODASFAFVALAVIFCCFLSMLLIFVPKVI 734
 Db 802 indhravgmamynvavclitapvtmllssqdaafafaalaivfsyitlvilvfpkmr 861
 QY 735 EVIRHP--KDAESKYNPDSAISKEDERYQKLVTEQLORLITQKEKIRVLRQLVE 792
 Db 862 rllrtgwgseaqdtkmtgssnnneeksrllkenrelekliaaeeervselrlqlrs 921
 QY 793 R 793
 Db 922 r 922

RESULT 9
 AAY83145
 ID AAY83145 standard; Protein; 960 AA.
 XX AC AAY83145;
 XX DT 24-JUL-2000 (first entry)
 XX DE Human GABAB1A receptor.
 XX KW GABAB1A receptor; G-protein; disease; treatment; detection;
 KW therapy; antibody; immune response; infection; cancer; diabetes;
 KW obesity; anorexia; bulimia; Parkinson's disease; heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; ulcers; asthma;
 KW allergy; benign prostatic hypertrophy; migraine;
 KW neurological disorders including anxiety; schizophrenia;
 KW depression; dementia; Huntington's disease;
 KW Gilles de la Tourette's syndrome.
 XX OS Homo sapiens.
 XX PN WO200012106-A1.
 XX PD 09-MAR-2000.
 XX PF 30-AUG-1999; 99WO-US19435.
 XX PR 01-SEP-1998; 98US-0144779.
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX PI Elshourbagy NA;
 XX DR WPI; 2000-237771/20.
 XX DR N-PSDB; AA293411.
 XX PT New GABAB1A polypeptide useful for diagnosis, treatment and prevention
 PT of diseases associated with its expression including infections,
 PT psychotic and neurological disorders and cancer
 XX PS Claim 1; Page 34-36; 38pp; English.
 XX CC The GABAB1A receptor is believed to be a member of the GABAB
 CC family of polypeptides. They are therefore of interest because
 CC members of the purinergic 7TM receptor family (G-protein coupled
 CC receptors) of genes are involved in a number of biological and
 CC disease manifestations. They are also a successful target for
 CC pharmaceutical intervention. Antibodies directed against GABAB1A
 CC and its peptides can be used to treat bacterial, fungal, protozoan
 CC and viral infections, pain, cancers, diabetes, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypotension, urinary retention, osteoporosis, angina pectoris,
 CC myocardial infarction, stroke, ulcers, asthma, allergies, benign
 CC prostatic hypertrophy, migraine, vomiting, psychotic and
 CC neurological disorders including anxiety, schizophrenia, depression,

CC dementia and severe mental retardation and dyskinesias such as
 CC Huntington's disease or Gilles de la Tourette's syndrome. The
 CC GABAB1A polypeptide or a vector comprising a sequence encoding the
 CC polypeptide can be used to induce an immunological response in a
 CC mammal to protect against disease. The presence or absence of a
 CC mutation in the nucleotide sequence encoding the GABAB1A polypeptide
 CC can be detected in the genome of a subject and/or the presence or
 CC amount of expression of the polypeptide in a sample from the subject
 CC can be analysed and used to diagnose a disease or susceptibility to a
 CC disease related to the expression or activity of GABAB1A.
 CC Diagnosis can be measured at the RNA level using nucleic acid
 CC amplification, e.g. polymerase chain reaction, RNase protection or
 CC Northern blotting or at the protein level by radioimmunoassay,
 CC competitive-binding assays, Western blot analysis or ELISA assays
 CC (enzyme linked immunosorbent assay).
 XX Sequence 960 AA;

Query Match 46.4%; Score 2030.5; DB 21; Length 960;
 Best Local Similarity 49.3%; Pred. No. 2.6e-192;
 Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLQGGVAGRPDE--LHIGGIFPIAGKGGWGGQACMPATRLALDDVKNQPNLPGFKLI 81
 Db 154 phcqvnrtphserravyigalfpms--ggwpqgacqpavemaiedvnsrrdiipdyelk 211
 QY 82 LHSNDSCEPCGLGASVMYLLNPKOKLMLLAGCSTCTTVAEAAKMMNLLVLCYGASSP 141
 Db 212 lihdsxcdpqqatkylyellyndpikilmpgscsvstlvaearmnnllvlysgsssp 271
 QY 142 ALSDRKRPFTLFRTHPSATVHNPTRIKLMKFGWSRVAILQQAAEEVFISTVEDLENROME 201
 Db 272 alsnrqfptftrhpsatvlhnpvrlkfwgwkkiatiqgttevfstdlleerkye 331
 QY 202 AGVEIVTRQSFSLDPTDAVRNLRQDARIIVGLFVVAARVRLVCEMYKQQLYGRAHWFF 261
 Db 332 agieitfrqsfspavpvknkrqdarilvglyfetearkvcevykerlfgkykvwfl 391
 QY 262 IGWYEDNWYEVNKAEGITCTVEQMRTAAEGHLTAALMNONNOTTISGMTAEFRHL 321
 Db 392 igwyadnwfkf--ydpnsinctvdemteavegnitteivmlnpantrsimtsqefvekl 449
 QY 322 NQALIEEGYDINHRYPE--GYQEAFLAYDAVMSVALAFNKTMRERLTGTGKSLRDTYIT 378
 Db 450 tkrl-----krhpeetggfqaepalaydaialalalanktsagggrsgvrlfedfyn 500
 QY 379 DKETADEIYAAMNSTQFLGSGVVAFFSSQGDRIALTQEQMDKGYEKLYGYDTOLDNLS 438
 Db 501 nqtitdqiyrannsssfegsvghvfdasgrmawtlieqlqggyskkygyvdstkddls 560
 QY 439 WLNTQEWIGGKVPQDRTIVTHVTRVSLPLFCVMCTISSCGIFVAFALIIENINKNHRRV 498
 Db 561 wskcdkwlgsgppadtvlvktfrlfsqklfsvsvslgvlavvcslfnlyushvry 620
 QY 499 IQSHHPVCNTLMLFGVITCLISVILLGDGRFVSPEEYPKICQARAWLLSTGFTLAYGAM 558
 Db 621 iqnsqpalnltavgcslalaavfplgidyghnrgnqpfvcqarlwlilgfgslgysgm 680
 QY 559 FSKVMVRHREFTTK--AKTDPKKKVEPKWLYTMVSGLLSIDLVILLSWIFDPLQRYLRTFF 616
 Db 681 ftkiwwhtvttkkeekewrktlepkwlyatvgllvgmdvltaiwqivdplhrtietf 740
 QY 617 PLEDPVSTDDIKIRPELHESORNSMWGLVYGFKGLIIVFLGFLAYETRSIKVKQIN 676
 Db 741 akeepkedi-dvslpqhccsskmmwtgifygkglililgflayetskystekin 799
 QY 677 DSRVVGSIYNNVLCITAPVGVVIASQODASFAFVALAVIFCCFLSMLLIFVPKVIEW 736
 Db 800 dhravgmamynvavclitapvtmllssqdaafafaalaivfsyitlvilvfpkmr 859
 QY 737 IRHP--KDAESKYNPDSAISKEDERYQKLVTEQLORLITQKEKIRVLRQLVER 793
 Db 922 r 922

PT New DNA encoding human and murine receptor subunits, useful for
PT identifying agonists and antagonists for treatment of depression,
PS epilepsy and neuropsychiatric disorders
XX
XX
XX Claim 11; Fig 18; 128pp; English.
XX
XX The present sequence represents a human gamma-amino-butyric acid (GABA)
CC B receptor (GABAR) subunit designated GABAR1a. The present invention
CC also describes the GABAR subunit designated HG20. Cells expressing
CC the new receptor subunits are useful for identifying GABAR agonists
CC and antagonists. HG20 proteins and their antagonists are useful for
CC inhibiting HG20 or GABAR function, useful for treating depression,
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
CC and central nervous system disorders.
XX
SQ Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
QY 24 PHLOGVAGRPDE--LHIGGIPIAGKGGWGGOGACMPATRLALDDVKNOPNLLPGFKLI 81
Db 155 phcqvnrtpsherravvigaifpms--ggwpggqacqavemaledvnsrrdlpdyelk 212
QY 82 LHSNDECEPGLGASVYMLLYNKPQKMLLAGCSTVCTTVAARAKMNLIVLCYGASSP 141
Db 213 lihndskdpqgatkyllylndpikilmpgcsstvlvaeaarmnllivlysgssp 272
QY 142 ALSDKRFPFTLRTHPSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDLENRCME 201
Db 273 alsnrqrfptfrthpsatvhnptrvklfekwgwkkiatigqtevtstlddleervke 332
QY 202 AGVEIVTROSEFSDPTDVAENLRDARIIVGLFYVVAARVLCVMYKQOLYGRAHWFF 261
Db 333 agieifrdgsfddpavpvnknrqdarliivfyetearkvficevykerlfgkkywfl 392
QY 262 IGWEDNWTVEVNLKARGICTVQMRIAARGHLTTALMNNQNTTISGMTAEFPHRL 321
Db 393 igwadnwfk--ydpisinctvdeameaveghitveimlpnpantrsismtsqefvekl 450
QY 322 NQALIEEGYDINHRYPE---GYOEAPLAYDAVMSVALAPNKTMRITTCCKSLRDFYTT 378
Db 451 tkrl-----krhpeetggfqaelaydaiwalalalnktsgggrsgvrledfayn 501
QY 379 DKEIADEIYAAMNSTOFLGSGVVAVSSQGDRIALTOIEOMIDGKYEKLGYDTQDNL 438
Db 502 nqdtidqiyramnsssfegvshvvdasgrmawtliedlqggykkgiyydstkdls 561
QY 439 WLNTQEWIGGKVPQDRTIVTHVLTSTVSLPLFVCMCTISSCGIFVAFALITFNWKKHRRV 498
Db 562 waktkwigsgppadqlviktfrfsqklfsvslssigvlavvclsfniynshvry 621
QY 499 IQSSHPVCNTIMLFGVVICILISVILLIDGRFVSPPEYPKICQARWLLSTGFTLAYCAM 558
Db 622 ignsqpnlnltaavgcslalaaavplgdghygrnqpfvccqarlwlglgfslygysm 681
QY 559 FSKWVRHREFTTK--AKTDPKKVPEWPKLYTMVSGLLSIDLVLLSQIFDPQRYLETFF 616
Db 682 ftkiwwhvftkkekewrktlepkvlyatvgllvgmdvltlalgwldpdlhrhtetf 741
QY 617 PLEDPVSTDDIKIRPELEHCESSORSMWGLVYGFKGLILVFLGLAYETRSIKVKQIN 676
Db 742 akeepedi-dvslpqlehcscrkmtwlgifyykglllgliflayecksvstekin 800
QY 677 DSRVYGMSIYNNVVLCLITAPGVMIASQDASFAFVALVIFCCFLSMLLIFPKVIEV 736
Db 801 dhravgmalylnavclitapvtmilssqdaafafaslaivfssytilvlfvpmrll 860
QY 737 IRHP--KDAESYNPDSAISKEDEERYKQLVTNEOQLRLITQKEKIRVLRORLVER 793
Db 861 itrgevwqseadtmktgssnnneeksrllkenrelekieakeervselrlqlqsr 919

RESULT 12
AAY14101
ID AAY14101 standard; Protein; 961 AA.
XX
XX AAY14101;
AC AAY14101;
XX
XX 21-JUL-1999 (first entry)
DT
XX Human GABAR receptor 1a protein sequence.
DE
XX
XX GABAR receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.
XX
XX Homo sapiens.
OS
XX
XX WO9921890-A1.
PN
XX
XX 06-MAY-1999.
PD
XX
XX 27-OCT-1998; 98WO-SE01947.
PF
XX
XX 17-JUL-1998; 98SE-0002575.
PR
XX 27-OCT-1997; 97SE-0003914.
PR
XX 16-MAR-1998; 98SE-0000864.
PR
XX (ASTR) ASTRA AB.
PA
XX
XX Ekstrand J;
PI
XX
XX WPI; 1999-302985/25.
DR
XX N-PSDB; AAX58054.
DR
XX
XX Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX
XX Claim 17; Page 79-84; 222pp; English.
PS
XX
XX This sequence is a human gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.
XX
XX Sequence 961 AA;
SQ

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
QY 24 PHLOGVAGRPDE--LHIGGIPIAGKGGWGGOGACMPATRLALDDVKNOPNLLPGFKLI 81
Db 155 phcqvnrtpsherravvigaifpms--ggwpggqacqavemaledvnsrrdlpdyelk 212
QY 82 LHSNDECEPGLGASVYMLLYNKPQKMLLAGCSTVCTTVAARAKMNLIVLCYGASSP 141
Db 213 lihndskdpqgatkyllylndpikilmpgcsstvlvaeaarmnllivlysgssp 272
QY 142 ALSDKRFPFTLRTHPSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDLENRCME 201
Db 273 alsnrqrfptfrthpsatvhnptrvklfekwgwkkiatigqtevtstlddleervke 332

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QY 202 AGVEIVTRQSFLSDPTDAVRNRRDARIIVGLFYVVAARRVCLCEMYKQOLYGRAHWFF 261
DB 333 agieitfrqsfspavpvknkrqdariivglfyetearkvfcevykerlfgkkywfl 392
QY 262 IGWYEDNWEVNLKAEITCTVEQMRIRAEGLHTTTEALMWNQNTTISGMAEERHRL 321
DB 393 igwyadnwfk1--ydpnsinctvdenteaveghittemlntpantrsisnmtsqefvekl 450
QY 322 NOALIEGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTMERLTGKKSLRDTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaivalalalnktsggggrsvrledfyn 501
QY 379 DKEIADEIYAAMNSTQFLGVSGWAFSSQGDRIALTQIEQMDIGRYEKLYGTYDTQDLNLS 438
DB 502 nqitdqiyrarnsssfegvshvfdasgrmawtlieqlggsgykygystkddls 561
QY 439 WLNTQEWIGGKVPQDRTIVTHVLRVSLPLFCVCMCTISCGIFVAFALIFINWKNHRRV 498
DB 562 wsktdkwiggspadqtlviktfrfksqklfsvslslgvlavvcslfniynshvry 621
QY 499 IQSSHVPVNTIMLFGVVICLSVILLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYGAM 558
DB 622 ignsqnlnhtavgsialaavfplgdyhignqpfvcqarlwlglgfslygysm 681
QY 559 FSKVMVRHRTTK--AKTDPKPKVWPRLYTMVSGLLSIDLVLLSQWTFDPLQRYLETF 616
DB 682 ftkiwwhtvtkkekewrktlepklyatvgilvgmdvltaiwqivdplhrtief 741
QY 617 PLEDPVSTDDIKIRPELEHESQSNMWGLVYGFGLILVFLVGLFAYETRSIKVKQIN 676
DB 742 akeepkedi-dvsilpqlhecssrkmmtwlgifygykglllllglflayetskvsstekin 800
QY 677 DSRVYGVMSIYNVVLCLITAPGVGVIASQODASFAVALAVIFCCFLSMLLIFVPKVIEW 736
DB 801 dhravgmalyvavclitapvtmllssqgdaafaslaivfssyitvlvfpkmrli 860
QY 737 IRHP--KDKAESKYNPDSAISKEDEERYQKLVTEQQLRQITQREKIRVLRQLRVER 793
DB 861 itrgewseadmtkgtstnnneeksrllekenrelektiaeeerveisrlhqlqr 919

RESULT 13
AA49133
ID AA49133 standard; Protein; 1323 AA.
XX
AC AA49133;
XX
XX 07-JAN-2000 (first entry)
XX
DE GABA-BRla*Gqo5 fusion construct protein sequence.
XX
KW G-protein fusion receptor; Car; calcium receptor; GluR; head injury;
KW metabotropic glutamate receptor; GABABR; chimeric receptor; stroke;
KW gamma-aminobutyric acid receptor; allosteric modulator; antagonist;
KW spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia;
KW Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
KW cognitive disorder.
XX
OS Homo sapiens.
XX
PN WO9951641-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07333.
XX
PR 03-APR-1998; 98US-0080671.
XX
PA (NPS-) NPS PHARM INC.
XX
PI Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JB;
PI SImin RT;
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XX
DR WPI; 1999-610995/52.
XX N-PSDB; AA231064.
XX
PT New G-protein fusion receptors and chimeras containing domains from
PT different receptors, used to screen for modulators, potentially useful
PT e.g. for treating or preventing stroke or Alzheimer's disease -
XX
PS Disclosure; Fig 14; 255pp; English.
XX
CC The invention relates to G-protein fusion receptors (I) comprising:
CC (1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and
CC intracellular (ICD) domains, each chosen independently from a Car
CC (calcium receptor), GluR (metabotropic glutamate receptor) and GABABR
CC (gamma-aminobutyric acid receptor); (2) an optional linker attached to
CC the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the
CC linker. (I), and recombinant chimeric receptors (CR) without the GP
CC component, are used to assess function of the various domains and to
CC identify compounds (e.g. allosteric modulators or antagonists) that act
CC on these domains. The modulators are potentially useful for treating or
CC preventing diseases associated with the receptors, e.g. stroke, head or
CC spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia,
CC Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive
CC disorders and depression. Nucleic acid (II) that encodes (I) is used:
CC (1) for recombinant production of corresponding proteins; and (2) to
CC produce cells used in screening for modulators. Use of Car and mGluR
CC domains allows presentation of GABABR domains, to a binding agent, in a
CC form more like the natural domain structure compared with use of
CC incomplete receptors, lacking one or more domains. By shuffling different
CC domains, agents can be identified that affect particular domains of a
CC receptor.
XX
SQ Sequence 1323 AA;
XX
Query Match 46.4%; Score 2030.5; DB 20; Length 1323;
Best Local Similarity 49.3%; Pred. No. 4.4e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
QY 24 PHLOGGVAGRPDE--LHIGGIFPIAGKGQGGQACQACMPATRLALDDVKNPGLPGFKLI 81
DB 155 phcqvnrtpshserravyigalfpms--ggwpgggacqavemaledvnrdilpdyelk 212
QY 82 LHSNDECEPGLGASVVMYLLNYPKOKMLLAGCSTVCTTVAAAKMNLVILCYGASSP 141
DB 213 lihhsdkcdpgqatkyellyndpkiilimpccssvstlvaaeamnmlivisygsssp 272
QY 142 ALSDRKRFPFLFRTHPSATVHNPNTRIKMKKFGWSRVAILQQAEEVFISTVEDIENRME 201
DB 273 alsnqrftptfthpsatihnptrvklfekwgwkkiatigqttevtstlddleervek 332
QY 202 AGVEIVTRQSFLSDPTDAVRNRRDARIIVGLFYVVAARRVCLCEMYKQOLYGRAHWFF 261
DB 333 agieitfrqsfspavpvknkrqdariivglfyetearkvfcevykerlfgkkywfl 392
QY 262 IGWYEDNWEVNLKAEITCTVEQMRIRAEGLHTTTEALMWNQNTTISGMAEERHRL 321
DB 393 igwyadnwfk1--ydpnsinctvdenteaveghittemlntpantrsisnmtsqefvekl 450
QY 322 NOALIEGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTMERLTGKKSLRDTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaivalalalnktsggggrsvrledfyn 501
QY 379 DKEIADEIYAAMNSTQFLGVSGWAFSSQGDRIALTQIEQMDIGRYEKLYGTYDTQDLNLS 438
DB 502 nqitdqiyrarnsssfegvshvfdasgrmawtlieqlggsgykygystkddls 561
QY 439 WLNTQEWIGGKVPQDRTIVTHVLRVSLPLFCVCMCTISCGIFVAFALIFINWKNHRRV 498
DB 562 wsktdkwiggspadqtlviktfrfksqklfsvslslgvlavvcslfniynshvry 621
QY 499 IQSSHVPVNTIMLFGVVICLSVILLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYGAM 558
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Db 622 iqnsqpnlnltavgcslalaavfplgldyghgrnqfvcqarlwlilglfslgygsm 681
Qy 559 FSKVVRVHRFTTK--AKTDPKKVPEWKLYMTVMSGLSLDLVLLSWQIPDPQRYLETF 616
Db 682 ftkiwwhtvftkkekewrktlepwklyatvllvgmdvltlailqivdpplrhtietf 741
Qy 617 PLEDVSTDDIKIRPELEHCHESQNSMWLGLVYGPFGKLLVFGFLAYETRSIKVKQIN 676
Db 742 akeepkedl-dvslilpqlehcscrkmtwlgfygkglilgliflayetksvstekin 800
Qy 677 DSRVYGMSTYNNVWLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFVPRKVIEW 736
Db 801 dhvargmainvavclitapvmtlssqqdaafafaslaivfssyitvllvfpkmrri 860
Qy 737 IRHP--KDKAESKYNPDSSAISKDEERYQKLVNTENBQLQRLITQKEKIRVLRLIVER 793
Db 861 itrgewqseqdmtgtsntnnneeksrllkenrelekiiaekeervselrhqlqsr 919

RESULT 14
AAW40117
ID AAW40117 standard; Protein; 793 AA.
AC AAW40117;
XX
DT 03-JUN-1998 (first entry)
XX
DE Human GABA-BR1a/b receptor protein.
XX
KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
XX
OS Homo sapiens.
XX
PN WO9746675-Al.
XX
PD 11-DEC-1997.
XX
PF 19-MAR-1997; 97WO-EP01370.
XX
PR 22-NOV-1996; 96US-0756091.
PR 30-MAY-1996; 96OS-0655716.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
XX
DR WPI; 1998-042183/04.
DR N-PSDB; AAV10265.
XX
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
XX
PS Claim 4; Page 62-67; 108pp; English.
XX
CC This sequence represents a novel human GABA-B receptor protein,
CC GABA-BR1a/b. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
XX
SQ Sequence 793 AA;

Query Match 46.4%; Score 2029.5; DB 19; Length 793;
Best Local Similarity 49.9%; Pred. No. 2.4e-192;
Matches 381; Conservative 151; Mismatches 211; Indels 21; Gaps 7;

Qy 37 LHIGGIFPIAGKCGWQGOQACMPATRLALDDVKNQPNLLPGFKLILHSNDECEPGLCAS 96
Db 2 vyigalipms--ggwpggacqpavemaledvnsrrdlpdqyelklhhsckdpggatk 59
Qy 97 VMYNLLYNKPKQLMLLAGCSTVCTTVAEAAKMMNLLVLCYGASSPALSDRRKFFTLPRTH 156
Db 60 ylyellyndpkiilimpqcsstvlvaearmmalilwlsygspsalsnqrftffrth 119
Qy 157 PSATVHNPTRIKLMKFGWSRVAILQOAAEEVFSTVEDLENRCMEAGVEIVTROSFLSDP 216
Db 120 psatlhnptrvkifekgwkkkatiqttevtftldlleervkeagleitfrgssfdp 179
Qy 217 TDVNRNLRQDARIIVGLFYVVAARRVLCEMYKOOLGGRHVFFIGYEDNWTNEVLKA 276
Db 180 avpknlnkrqgdariivglfyetearkvfcevkerlfgkyvwflgwyadnwfk--yd 237
Qy 277 EGTCTVEQRIAAEGHLLTTEALMWNQNNOTTISGMTAAEERHRLNQAALIEEGYDINH 336
Db 238 psinctvdmetaveghitfeivmnpantrsisnmtsqefvekltrl-----kr 288
Qy 337 YPE---GYEAPLAYDAVMSVALAFNKTMERLTTGKSLRDFYTDKEIADIEIYAAMNST 393
Db 289 hpeetggfqaeplaydaiwalalnhtksgggrsgvrledfnynntitdqiyramnss 348
Qy 394 QFLGVSGVAFPSOGDRIALTQIEOMIDGKYEKLYGYDTQDLNLSWLNTEQWIGKVPQD 453
Db 349 sfegvsghvvdasgsrmawtlieqlggsgykgkgydstkddlsksktdkwigsspad 408
Qy 454 RTIVTHVLRTVSLPLFCVCMCTISSCGIFVAFALIIFNINWKNHRRVIOSSHVPVCNTIMLFG 513
Db 409 qtlviktrflsqklfissvslsllgvlavvcisfnlshvryiqnsqpnlnltav 468
Qy 514 VIICLISVILGLIDGRFVSPPEYPKICOARAWLLSTGFTLAYGAMFSKVRVHRFTTK-- 571
Db 469 csialaavfplgldyghgrnqfvcqarlwlilglfslgygsmftkiwvhtvftke 528
Qy 572 AKTDPKKVPEWKLYMTVMSGLSLDLVLLSWQIPDPQRYLETFPLEDPVSTDDIKIR 631
Db 529 ekewrktlepwklyatvllvgmdvltlailqivdpplrhtietfakeepkedl-dvslil 587
Qy 632 PELEHCHESQNSMWLGLVYGPFGKLLVFGFLAYETRSIKVKQINDSYGMSIYNNVVL 691
Db 588 pqlhcscrkmtwlgfygkglilgliflayetksvstekindhravgmalyav 647
Qy 692 CLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFVPRKVIEWIRHP--KDKAESKYN 749
Db 648 clitapvmtlssqqdaafafaslaivfssyitvllvfpkmrriitrgewqseqdmtk 707
Qy 750 PDSAISKEDEERYQKLVNTENBQLQRLITQKEKIRVLRLIVER 793
Db 708 tgsstnnneeksrllkenrelekiiaekeervselrhqlqsr 751

RESULT 15
AAV14109
ID AAV14109 standard; Protein; 892 AA.
XX
AC AAV14109;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor lg protein sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy;
KW alternative splicing; isoform.
XX
OS Homo sapiens.
XX

PN WO9921890-A1.
XX 06-MAY-1999.
XX 27-OCT-1998; 98WO-SE01947.
XX 17-JUL-1998; 98SE-0002575.
XX 27-OCT-1997; 97SE-0003914.
XX 16-MAR-1998; 98SE-0000864.
XX (ASTR) ASTRA AB.
XX Ekstrand J;
XX WPI; 1999-302985/25.
XX N-PSDB; AAX58064.
XX Polynucleotides encoding human and canine gamma aminobutyric acid
XX type B receptors, used to screen for compounds that are inhibitors
XX of transient lower oesophageal sphincter relaxations
XX Example 7; Page 176-181; 222pp; English.
XX This sequence is an isoform of a human gamma aminobutyric acid
XX type B (GABAB) receptor of the invention, created by alternate splicing.
XX Nucleic acid molecules encoding GABAB receptors can be used to screen for
XX compounds that are inhibitors of transient lower oesophageal sphincter
XX relaxations (TLRSR). They can also be used to screen for agonists or
XX antagonists of the GABAB receptors. Inhibitors of TLRSR are useful for
XX treating gastro-oesophageal reflux disease. Other uses of GABAB
XX receptors, such as human GABAB Ric or 1d, comprise diagnosis or treatment
XX of conditions related to GABAB dysfunction, e.g. epilepsy, psychiatric
XX disorders, emesis, irritable bowel syndrome, dyspepsia, spasticity,
XX arthritis, allergies, autoimmune diseases, neoplastic diseases, pain and
XX infectious disease.
XX Sequence 892 AA;

Query Match 46.4%; Score 2029.5; DB 20; Length 892;
Best Local Similarity 49.9%; Pred. No. 2.9e-192;
Matches 381; Conservative 151; Mismatches 211; Indels 21; Gaps 7;

QY 37 LHIGGIFPIAGKGQGGQACMPATRLALDDVKNQPNLLPGFKLILHNSDSECEPLGLAS 96
Db :||: ||||: || ||||| || :||: ||| :||: ||| :||: ||| :||: |||
101 vyigalfms--ggwpgggacqpavemaledvnsrrildpuyelklnhdsckdpggatk 158
QY VMYNLLYNKPKMLLAGCSVCTTVAEAKMWNLLVLCYGASSPALSDRKRFPFLFRTH 156
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
159 ylyellyndpikilmpgcssvstlvaeaaarwnlvisyggsspalnsrqrptffrth 218
QY 157 PSAIVHNPTRIKLMKFGWSRVAILQOAEVFIETVEDLENRCMEAGVEIVTRQSFSDP 216
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
219 psatlnhptrvkllfkgwkxiatiqgttevtftldleervkeagieitfrgsfddp 278
QY 217 TDVNRLLRRDARIIVGLFVYVVAARRVLCMEYKQOLYGRAHWRFPGIWNEDNNYEVNLKA 276
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
279 avpknkkrqdarliivgfetearkvfeykerlfgkkyvwllygwyadnwfk1--yd 336
QY 277 EGITCTVEOMRIAAEGHLTTEALMWNQNNQTTISGMTAEFPRHRLNQALIERGYDINHNR 336
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
337 psinctvdmteaveghitteivmlnpantrsisnmtsqefvekitkrl-----kr 387
QY 337 YPE--GYOEAPLAYDAVWSVALAFNKTMRLETTGKSKSLRDFTYTPDKIEADIYAMNST 393
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
388 hpeetggfgeaplaydaiwalalalnktsgggrsgvrledfnynnqitdgiyramnss 447
QY 394 QFLGSGVWAPSSQGDRIALQIEQIDGKYELGYDYDTQLDNLNLWLNTEQWIGKVPQD 453
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
448 sfegvshvfdasgsrmawlleqlggsgykgigydytdkdlswsktdkwigspbad 507
QY 454 RTIVTHVLRVTSPLFVCMCTISSCGIFVAFALIFNINWKNHRRVIOSSHPVCNTIMLFG 513
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||

Db 508 qtlviktfrflsqklfisvsvlsslglvavvcslsfniynshvryiqsqnlnnltavg 567
QY 514 VIICLSIVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGAMFSKVRVHRFTTK-- 571
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
568 csialaavfplgdgyhigrnqfpvcqarllwllglsfgysgmftkiiwwhtvtfckke 627
QY 572 AKTDPKKKVEPWKLYTWVSGLLSIDLVILLSWQIFDPLQRYLFTFFPLEDPVSTDDIKIR 631
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
628 ekkewrktlepwklyatvgllvgmdvltlaigwldvplhrtietfakeepkedi-dvsil 686
QY 632 PELEHCESORNSMWLGLVYGFKGLILVFGFLAYETRSIKVKQINDSRVYGMSTYNNVVL 691
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
687 pqlhecssrkmntwlgifygykglllllglflayetksvstekindhavgmalynavl 746
QY 692 CLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFVPKVEIVIRHP--KDKAESKYN 749
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
747 clitapytmilssqdaafafaslaivfssyitlvilfvpkmrlitrgewqseqadtmk 806
QY 750 PSDAISKEDEERYOKLVTENEQLORLITQKEEKIRVLRQRLVER 793
Db :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||
807 tgsstnnneeeksrlllekenrelekiiaekeervselrhqlqsr 850

Search completed: April 30, 2002, 10:13:05
Job time: 127 sec

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 19, 2002, 10:51:08 ; Search time 19 Seconds
(without alignments)
1300.803 Million cell updates/sec

Title: US-09-715-962-2

Perfect score: 4374

Sequence: 1 MRKDMTSDGAVTFWIFLLCL.....LINSAHATPAATLAITQGE 840

Scoring table: BLOSUM62.

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCrUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2035	46.5	844	4	US-09-422-936-51
2	2034.5	46.5	899	4	US-09-422-936-71
3	2032	46.5	844	4	US-09-422-936-47
4	2031.5	46.4	964	4	US-09-422-936-53
5	2030.5	46.4	961	4	US-09-422-936-49
6	2029.5	46.4	892	4	US-09-422-936-75
7	2029.5	46.4	960	4	US-09-422-936-45
8	1967	45.0	886	4	US-09-422-936-77
9	1209.5	27.7	461	4	US-09-422-936-57
10	1206	27.6	581	4	US-09-422-936-59
11	1205	27.5	578	4	US-09-422-936-55
12	1158.5	26.5	859	3	US-09-183-253-2
13	1072.5	24.5	496	4	US-09-422-936-85
14	1033	23.6	563	4	US-09-422-936-79
15	697.5	15.9	332	3	US-09-183-253-4
16	359	8.2	908	4	US-08-855-146-2
17	355.5	8.1	908	3	US-08-823-110-1
18	355.5	8.1	908	3	US-08-604-298-1
19	355	8.1	915	4	US-08-617-785-12
20	355	8.1	922	4	US-08-617-785-14
21	353	8.1	912	4	US-08-617-785-2
22	353	8.1	912	4	US-09-641-318-2
23	353	8.1	915	1	US-08-453-862-2
24	353	8.1	915	2	US-08-452-734A-2
25	353	8.1	915	4	US-08-176-401B-2
26	353	8.1	915	5	PCT-US94-14989-2
27	349.5	8.0	912	5	PCT-US91-09422-19

28	328	7.5	879	1	US-08-072-574-6	Sequence 6, Appli
29	328	7.5	879	1	US-08-486-270-6	Sequence 6, Appli
30	328	7.5	879	3	US-08-367-264-6	Sequence 6, Appli
31	328	7.5	879	4	US-09-153-757-6	Sequence 2, Appli
32	327	7.5	872	3	US-08-337-797A-2	Sequence 2, Appli
33	327	7.5	872	3	US-09-258-523-2	Sequence 2, Appli
34	323	7.4	879	4	US-08-794-158-2	Sequence 2, Appli
35	321.5	7.4	867	4	US-08-617-785-4	Sequence 2, Appli
36	313.5	7.2	877	2	US-08-407-875-2	Sequence 2, Appli
37	313.5	7.2	877	4	US-09-277-858-2	Sequence 2, Appli
38	311.5	7.1	877	3	US-09-126-280-2	Sequence 2, Appli
39	302.5	6.9	1180	4	US-08-660-148-2	Sequence 2, Appli
40	297.5	6.8	1212	4	US-08-660-148-5	Sequence 5, Appli
41	283.5	6.5	1180	1	US-08-486-270-8	Sequence 8, Appli
42	283.5	6.5	1180	3	US-08-367-264-8	Sequence 8, Appli
43	283.5	6.5	1180	4	US-09-153-757-8	Sequence 8, Appli
44	282.5	6.5	1180	1	US-08-072-574-8	Sequence 8, Appli
45	281	6.4	856	4	US-09-619-353-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-422-936-51

; Sequence 51, Application US/09422936

; Patent No. 6465213

; GENERAL INFORMATION:

; APPLICANT: Ekstrand, Jonas

; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES

; FILE REFERENCE: 06275-165002

; CURRENT APPLICATION NUMBER: US/09/422,936

; CURRENT FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: US 09/242,608

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: PCT/SE98/01947

; PRIOR FILING DATE: 1998-10-27

; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

; PRIOR FILING DATE: 1997-10-27

; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2

; PRIOR FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2

; PRIOR FILING DATE: 1998-07-17

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 51

; LENGTH: 844

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-422-936-51

Query Match

Best Local Similarity 46.5%; Score 2035; DB 4; Length 844;

Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;

QY	23	SPHL---QGVACRPDE---LHIGGIFTAGKGGWGOACMPATFLALDDVKNPQLL	75
DB	32	SPHLPHSRKVPHPHSERRAVYIGALFPMSS--GGPPGGACQCPAVEMALEDVNSRRDIL	89
QY	76	PGFKLHNSDSCEPGLGASVMYLNLYNKPQKMLIAGCTVCTTVAEAAKMNLIIVLC	135
DB	90	PYELKLIHSDKCDPQATKYLIELLYNDPIKILMPGSSVSTLVAAEARNMLIVLS	149
QY	136	YGASSPALSDRKRPFTLFRTHPSATVHNPTRIKMLKFGWSRVAILQQAEVISTVEDL	195
DB	150	YGSSSPALSNRQRPFTFRTHPSATLHNPTRVKLFEGWKWKIATIQOTTEVFTSLDDL	209
QY	196	ENRCMEAGVEIVTRQSFSLDPTDAVNLRRQDARIIVGLFYVVAARVCEMTKQQLYGR	255
DB	210	EERVKEAGEITFRQSFPSDPVAPVFNKLKRDARIIVGLFYETEARVCEVYKRLFGK	269
QY	256	AHWVFFIGVYEDNWYEVNKLKAEIGITCTVQMRTAAEGHLLTEALMNQNNQTTISGMTAE	315

; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-422-936-47

Query Match 46.5%; Score 2032; DB 4; Length 844;
Best Local Similarity 49.1%; Pred. No. 7e-198;
Matches 388; Conservative 151; Mismatches 213; Indels 38; Gaps 9;

QY 23 SPHLOGGAGRPD-----ELHIGGIFPIAGKGGWGGGACMPATRLALDDVKNK 70
DB 32 SPHLP-----RPHRPVPHSPSSERRAVYIGALFPMs--GGWPGGACQAPVEMALDVNS 84
QY 71 QPNLLPGFKLLIHSNDSCEPGLGASVMNLYNKPQKMLLAGCSTVCTTVAEAAKMN 130
DB 85 RRDLPDYELKLIHSDKCPQATKYLYELLYNDPIKILMPGCGSSVSTLVAEAAKMN 144
QY 131 LIVLCYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKLMKFKGSRVAILQOAEVEFVS 190
DB 145 LIVLSGSSSPALSNRQRPFTFRTHPSATLHNPTRVKLFKRWGKKIATIQOTTEVFTS 204
QY 191 TVEDLENRCEAGVEIVTRQSFSLDPTDAVRNLRQDARIIVGLFVVAARVLCMEYKQ 250
DB 205 TLDDLEERVKEAGIEIFTRQSFSDPAVPVKNLQKDARIIVGLFYEAEKRVCEVYKE 264
QY 251 QLYGRAHVFFPIGWEDNWYEVNKAEGITCTVEQMRITAAEGHLTEALMNNQNTTIS 310
DB 265 RLFGKKYVWFLIGYADNWFKT--YDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSTS 322
QY 311 GMTAEERHRLNQLIEBGYDINHDPYR--GYQEAFLAYDAVMSVALAFNKTWERLTT 367
DB 323 NMTSQEFVEKLTURL-----KRHPETGGFQEAFLAYDAIWAALALANKTSGGGGR 373
QY 368 GKSLRDTFTYDKETADEIYAAMNSTQFLGVSQGVVAFSSQGDRIALTQEQMIDKYEKL 427
DB 374 SGVLEDFNYNNQITDOIYRAMNSSSEFVGHVVDASGRMAWTILIEQLQGSYKKI 433
QY 428 GYDTQDLNLSWLNTEQWIGKVPQDRITVTHVLTSLPLFVCMCTISSCGIFVAFALI 487
DB 434 GYDSTKDDLSWSKTDKWIIGSPADQTLVTKTRFSLQKLFISVSVLSLGLVLAIVCL 493
QY 488 IFNWNKRRVIOSSHPCVNTIMLFGVILICLSVLLGIDGRFVSPEEYKPCQARALL 547
DB 494 SFNLYNSHVRVIONSQPNLNLTAVGCSLAAAVFPLGLDGYHIGRSQFPFVQCARLML 553
QY 548 STGFTLAYGAMFSKVRVHRFTTK--AKTDPKKKVEPKLTYMWSGLSIDLVLISWQI 605
DB 554 GLGSLGSGNFTKIWWVHTVFTKEEKEKWKRLTEPKLTYTGLLVGMVLTALQW 613
QY 606 FDPQRYLETFLPEDPVSTDDIKIRPELEHCESSQNMWGLVYGFKGLILVFLGLAY 665
DB 614 VDLHRTIETFAKEPKEDI-DVSLPQLEHCCSKKMTNLGIFGYKGLLLGLIFLAY 672
QY 666 ETRSIKVKQINDSRVYMSIYVNVVLCITAPGVMSVIAQQDASFAFVALAIVFCFLSM 725
DB 673 ETKSVSTEKINDHRAVGMAIYNAVLCITAPVTMILSQDAAAFASLAIVFSSYTL 732
QY 726 LLFVPKPVIEVIRHPKDAESK--YNPDSATSKDEERYOKLVTENEOLRLITKEBKI 783
DB 733 VLFVPMRRLITGEGWQSTQDTMKGSTNNNEEKSRLLENRELEKIIEKERV 792
QY 784 RVLRLQRLVR 793
DB 793 SELRHQLQSR 802

RESULT 4
US-09-422-936-53

; Sequence 53, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-422-936-53

Query Match 46.4%; Score 2031.5; DB 4; Length 964;
Best Local Similarity 49.4%; Pred. No. 1e-197;
Matches 386; Conservative 152; Mismatches 216; Indels 27; Gaps 9;

QY 24 PHLOGGAGRPD-----LHIGGIFPIAGKGGWGGGACMPATRLALDDVKNQNLPLPGFK 79
DB 158 PHCQ--VSRTPHSERRAVYIGALFPMs--GGWPGGACQAPVEMALDVNSRRDILPDYE 213
QY 80 LLIHSNDSCEPGLGASVMNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIIVLCYGAS 139
DB 214 LKLIHSDKCPQATKYLYELLYNDPIKILMPGCGSSVSTLVAEAAKMNLIIVLSYGS 273
QY 140 SPALSDRKRPFTLFRTHPSATVHNPTRIKLMKFKGSRVAILQOAEVEFISTVEDLENRC 199
DB 274 SPALSNRQRPFTFRTHPSATLHNPTRVKLFKRWGKKIATIQOTTEVFTSTLUDDLEERV 333
QY 200 MEAGVEIVTRQSFSDPTDAVRNLRQDARIIVGLFVVAARVLCMEYKQKLYGRAHV 259
DB 334 KEAGIEITRQSFSDPAVPVKNLQKDARIIVGLFYEAEKRVCEVYKELFGKKYVW 393
QY 260 FIGWEDNWYEVNKAEGITCTVEQMRITAAEGHLTEALMNNQNTTISGMTAEFRH 319
DB 394 FLIGWYADNWFKT--YDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSTSINMTSQEFVE 451
QY 320 RLNOALIEBGYDINHDPYR--GYQEAFLAYDAVMSVALAFNKTWERLTTGKKSRLDFT 376
DB 452 KUTRL-----KRHPETGGFQEAFLAYDAIWAALALANKTSGGSRGSRVRLDEFN 502
QY 377 YTDKETADEIYAAMNSTQFLGVSQGVVAFSSQGDRIALTQEQMIDKYEKLYGYDTQLDN 436
DB 503 YNNQITDOIYRAMNSSSEFVGHVVDASGRMAWTILIEQLQGSYKKIYGYDSTKDD 562
QY 437 LSWLNTEQWIGKVPQDRITVTHVLTSLPLFVCMCTISSCGIFVAFALIININKNHR 496
DB 563 LWSKTDKWIIGAPPADQTLVTKTRFSLQKLFISVSVLSLGLVLAIVCLSNFINSHV 622
QY 497 RVIOSSHPCVNTIMLFGVILICLSVLLGIDGRFVSPEEYKPCQARALLSTGFTLAYG 556
DB 623 RYIONSQPNLNLTAVGCSLAAAVFPLGLDGYHIGRSQFPFVQCARLMLLGLGSLGY 682
QY 557 AMFSKVRVHRFTTK--AKTDPKKKVEPKLTYMWSGLSIDLVLISWQIFDPLQRYLE 614
DB 683 SMFTKIWWVHTVFTKEEKEKWKRLTEPKLTYTGLLVGMVLTALQWVDPDLHRTIE 742
QY 615 TFLPEDPVSTDDIKIRPELEHCESSQNMWGLVYGFKGLILVFLGLAYETRSIKVKQ 674
DB 743 TFAKEEPKEDI-DVSLPQLEHCCSKKMTNLGIFGYKGLLLGLIFLAYETKSVSTEK 801

Qy	277	EGICTVEQMRIAEAGHLITTEALMWNQNNOTTISGMTAEFEHRHLNQALIERGYDINHDR	336
Db	337	PSINCTVDENTEAVEGHITTEIVMLNPANTRISNNTSQEFVEKLTKRL-----KR	387
Qy	337	YPE--CYQCAPLAYDAVWSALFAKNTWBLRTTGGKSLRDTFTYTDKETADEIYAAMNST	393
Db	388	HPETGGFQCAPLAYDAIWALALANKTSGGGRSGVRLEDFNYNQTTDQIYRAMNSS	447
Qy	394	QFLGVSGWAFSSOGDRIALQTEQMIDGKYEKLGVDYDQDNLNLNLTDEOMTIGGRVPOD	453
Db	448	SFECVSGHVVDAGSGEMAWTLLEQLOGSKYKGIYDSTKDDLWSKTDKWIIGSGPPAD	507
Qy	454	RTIYTHVLRVTSPLFCVMCTISSCGIFVAFALIIFNWNKHRRVYIQSSHPVCNITMLFG	513
Db	508	QTLVKTFRFLSKLFTISVSVLSSGLIVLAVVCLSENINSHVRYIQNSQPNLNLITAVG	567
Qy	514	VIICLSVILLGIDGRVSPDEEYPKTCQARAWLLSGTFTLAYGAMPSKVWRVHRFTTK--	571
Db	568	CSTLAAVFPGLGDYHGIRNQBPFFCQARLWLLGLGFLSGYGSMTFKWVHTVFTKKE	627
Qy	572	AKTDPPKKVPKLYTMVSGLLSIDLVLLSQIDFPLQRYLETFFLEDPVSTTDDIKR	631
Db	628	EKEWRKTLPEPKLYATVGLLVGMVDVLTAIWOVDPLHRTIETFAKEEPEKDI-DVSUL	686
Qy	632	PELEHESQRNSMWGLVYGFKGLILVGLFLAYETRSIKVQINDSRVVGMSIYNNVVL	691
Db	687	PQLEHCSRRKNTWLGIFYGKGLLLGLIFLAYETKSVSTEKINDHRAVGMAIYNVAVL	746
Qy	692	CLITAPGVMIASQQDASFAFVAIVFCFLSMLLIFVPKIVIEVIRHP--KDKAESKN	749
Db	747	CLITAPVTMLSSQQDAAFASIAIVFSSYITLVLFVFPKMRRLITRGWQSEADTMK	806
Qy	750	PDSAISKEDERTQKLVTENEQORLITQKEEKIRVLORLVER	793
Db	807	TGSTNNNEEKEKRLKEKENELEKJITAEKEERVSELRHQLOQR	850

RESULT 7

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US-09-422-936--45
; Sequence 45, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-422-936--45

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Qy	82	LHSNDSECEPGLGASVVMYNNLKNPKQKMLLACGCVTCTTVAEAAKMWNLVLVCYGASSP	14
Db	212	LIHSDSCDPCQATKYLYELLYNDPIKILMPGCCSVSTLVAEAAKMWNLVLVSGSSP	271
Qy	142	ALSDRKRPPLFRTHPSATVHNPTRIKMKKFGWSRAVILQOAEVFIPTVEDLENRCME	201
Db	272	ALSNRQRPFTFRTHPSATVHNPTRIKMKKFGWSRAVILQOAEVFIPTVEDLENRCME	331
Qy	202	AGVEIVTRQSGFLSDPTDAVNLNRQDARIIVGLVYFVVAARRVLCENYKQOLXGRAHVWF	261
Db	332	AGIEITTRQSGFFSDPAVPVNLNRQDARIIVGLVYFVVAARRVLCENYKQOLXGRAHVWF	391
Qy	262	IGWYEDNMYEVLNKAEGITCTVEQMRIAABEGHLLTEALMMNNQNTTISGMTAEFFRHL	321
Db	392	IGWYADNWKFT--YDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSISNMTSQEVEKL	449
Qy	322	NQALIEGYDINHDDRYPE---GYOEAPLAYDAVMSVALAFNKTMRKLTGKSKSLRDFYTV	378
Db	450	TKRL-----KRHPEETGGQEAPLAYDAIWALALANKTSGGGSGVRLIEDFN500	500
Qy	379	DKETADBIYAAMNSTQPLGVSQVVAFFSSQGDRTALTQIEMIDGKYEKLYGYDVTQLDNLS	438
Db	501	NQTTIDQIYRAMNSSSEFSGVHVFDAAGSRMAWTLIEQLQGGSYKKIYGYDSTKDDLS	560
Qy	439	WLNTQEWIGGKVPQDRTIVTHLVTRVSLPLFCVCMCTISSCGIFVAFALIIENWNKHRRV	498
Db	561	WSKTDKMGWGGSPADQPLVTKTRFISQKLFISVSLSSLGIVLVVCSFNLIYNHVRV	620
Qy	499	IQSSHPVCNTIMLFGVITICLISVILLIGDGRFVSPEYPRKICQARAWLLSTGFTLAYGAM	558
Db	621	IQNSOPNNLITAVGCSLAAVFPGLDGYHIGRSQFPVCOARLWLLGLGSLGYSYM	680
Qy	559	FSKVMVRHRTTK--AKTDPKKVPEPKLYMTVYSGLLSIDLVLLSWQIFDPLQRYLETF	616
Db	681	FTKIWWVHTVTRKEEKKERKLTLEPKWLYATVGLLVGMVLTALWQIVDPLHRTIET	740
Qy	617	PLEDPVSTDDIKIRPLEHCESSQRNSMWGLVYVGFKGLILVFLGFLAYETRSIKVQKIN	676
Db	741	AKEEPPKEDI-DVSLPQLCHSCSKMNTWIGIFYKGLLLGIFLAYETKSVSTEKIN	799
Qy	677	DSRVGMSIYNNVVLCLITAPVGMVITASQODASFVAVLAVIFCCFLSMILFVPKVIEV	736
Db	800	DHRVAGMAIYNVAVCLITAPVMTVILSSQODAAFASIAIVPSSYITIVLVFVPMRRL	859
Qy	737	IRHPKDAESK--YNPDSAISKEDERYQKLVTFENBQLQRLITQKBEKIRVLQRBLVER	793
Db	860	ITRCWQSEQTQDMTKTGSSTNNNEEKSRLLEKENLELEKIITAEKERYSELRHQLOSR	918
RESULT 8			
US-09-4222-936-77			
; Sequence 77, Application US/094222936			
; Patent No. 6465213			
; GENERAL INFORMATION:			
; APPLICANT: Ekstrand, Jonas			
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES			
; FILE REFERENCE: 06275-165002			
; CURRENT APPLICATION NUMBER: US/09/422,936			
; CURRENT FILING DATE: 1999-10-22			
; PRIOR APPLICATION NUMBER: US 09/242,608			
; PRIOR FILING DATE: 1999-02-19			
; PRIOR APPLICATION NUMBER: PCT/SE98/01947			
; PRIOR FILING DATE: 1998-10-27			
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2			
; PRIOR FILING DATE: 1997-10-27			
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2			
; PRIOR FILING DATE: 1998-03-16			
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2			
; PRIOR FILING DATE: 1998-07-17			
; NUMBER OF SEQ ID NOS: 85			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 77			

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; LENGTH: 886
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-422-936-77

Query Match          45.0%; Score 1967; DB 4; Length 886;
Best Local Similarity 48.0%; Pred. No. 3.3e-191;
Matches 375; Conservative 152; Mismatches 215; Indels 40; Gaps 8;

QY 19 CLTASPHLQGGVAGRDELHIGGIFPIAGKGGWGGQACMPATRLALDDVKNQPNLLPGF 78
Db 96 CVNRPHSERRA-----VIGALF-----PAMEALEDVNSRRDILPDY 134
QY 79 KILHNSDSECPGLGASVYNNLLYNKPKMLLAGCSTVCTTVAEAAKMNLLIVLCYGA 138
Db 135 ELKLIHDSKCDPGQATKYLYELLYNDPIKIILMPGCSVSTLVAEAAKMNLLIVLSYGS 194
QY 139 SPALSDRRKRPPTLFRTHPSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDLNR 198
Db 195 SSPALSNRQRFPTFRTHPSATLHNPTRVKLFPEKWKKIATIQOTTEVFTSLDLEER 254
QY 199 CMEAGVEIYVTSRFLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCCEMKQOOLYGRAHV 258
Db 255 VKEAGIEITFRGFSFSDPAVPVKNLKQDARIIVGLFYETEARKEVCEVTKERLFGKKYV 314
QY 259 WFFIGWEDNWEVNLKAEGITCTVBMKRIAAEGHLTTEALMNNQNTTISGMTAEFR 318
Db 315 WELIGWADNWEKI--YDPSINCTVDETEAVEGHITTEIVMLNPANTRISNMTSQEFV 372
QY 319 HRLNQALIEEGYDINHDPY--GQOEAPLAYDAVWSVALAENKMKMERUTTKKSLRDF 375
Db 373 EKLTKRL-----KRHEETGGFQEAPLAYDAIWAALALNLTSGGGGRSGVRLDEF 423
QY 376 TYTDEIADEIYAAMNSTOFLGVSQVAFSSQGDRIALTQIEQMIDGKYEKLGYDFTOLD 435
Db 424 NTNNQITQIYRAMSSSEFGVGHVFDASGRMAWTLIEQLQGSYKKGITYDSTKD 483
QY 436 NLSWLNTEQWIGKVPQDRITVTHVLTSLPLFVCMCTISSGIFVAFALIIFNWNKH 495
Db 484 DLSWKTDRWIGSPADQTLVTKTFRFLSQKLFISVSVLSLGIVLAVCLSFNINSH 543
QY 496 RVIQSHPVNCTIMLFGVVICILISVILGIDGRFVSPPEYKICQARAWLLSTGFTLAY 555
Db 544 VRYIONSQPNLNLTAAGCSLAAVAPFLGLDGYHIGRNOFPFVQCARLLGLIGFSLGY 603
QY 556 GAFSKVWVHRETKR--AKTDPKKEVPKLYTMVSGLLSIDLVILLSHQIDPLQRYL 613
Db 604 GSWFTKIWWVHTTKKEKKEWRKTELPWKLYATVGLLVGMDVLTALWQIVDPLHRTI 663
QY 614 ETPPLEDPVSTTDKIRPELEHCESSORNSMWLGLVYGFKGLIILVFLFLAYETRSIKVK 673
Db 664 EYFAKEEPREDI-DVSILPQLEHCSRRKMTWLGIFYGKLLLLGIFLAYETKSYSTE 722
QY 674 QINDSYGMSYNNVVVLCITAPGVMTIASQODASFAFVALAVIFCCFLSMLLIFVPKV 733
Db 723 KINDHRAVGMAIYNVAVLCITAPVTMILSSQODAAFAFASLAIVFSYITLVVLFVPKM 782
QY 734 IEVIRHP--KDKAESYNPDSALSKEDEERYQKLVTEQOLRLITOKEKIRVLRORLV 791
Db 783 RRLITRGEOAQDTMTKGSSTNNNEEKSRLLEKENRELEKIIAEKEERSVSELHQQL 842
QY 792 ER 793
Db 843 SR 844

RESULT 9
US-09-422-936-59
; Sequence 59, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
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FILE REFERENCE: 06275-165002
CURRENT APPLICATION NUMBER: US/09/422,936
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: US 09/242,608
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: PCT/SE98/01947
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
PRIOR FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-422-936-59

Query Match          27.7%; Score 1209.5; DB 4; Length 461;
Best Local Similarity 53.2%; Pred. No. 2.1e-114;
Matches 231; Conservative 73; Mismatches 107; Indels 23; Gaps 6;

QY 23 SPHL---QGGVAGRPDE---LHIGGIPPIAGKGGWGGQACMPATRLALDDVKNQPNLL 75
Db 32 SPHLPRPHSRVPHPPSSERRAVIIGALFPMS--GWPGGQACQPAVEMALEDVNSRRDIL 89
QY 76 PGFKLIHNSDSECPGLGASVYNNLLYNKPKMLLAGCSTVCTTVAEAAKMNLLIVLC 135
Db 90 PDYELKLIHDSKCDPGQATKYLYELLYNDPIKIILMPGCSVSTLVAEAAKMNLLIVLS 149
QY 136 YGASSPALSDRRKRPPTLFRTHPSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDL 195
Db 150 YGSSPALSNRQRFPTFRTHPSATLHNPTRVKLFPEKWKKIATIQOTTEVFTSLDLDL 209
QY 196 ENRCMEAGVEITVTRQSFLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCCEMKQOOLYGR 255
Db 210 EERYKEAGIEITFRGFSFSDPAVPVKNLKQDARIIVGLFYETEARKEVCEVTKERLFGK 269
QY 256 AHVWFFIGWEDNWEVNLKAEGITCTVBMKRIAAEGHLTTEALMNNQNTTISGMTAE 315
Db 270 KYVWFLIGWADNWEKI--YDPSINCTVDETEAVEGHITTEIVMLNPANTRISNMTSQ 327
QY 316 EFRHRLNQALIEEGYDINHDPY--GQOEAPLAYDAVWSVALAENKMKMERUTTKKSL 372
Db 328 EFVEKLTAKRL-----KRHEETGGFQEAPLAYDAIWAALALNLTSGGGGRSGVRL 378
QY 373 RDTYTDKEIADEIYAAMNSTOFLGVSQVAFSSQGDRIALTQIEQMIDGKYEKLGYDFT 432
Db 379 EDFNYNNGTITDQIYRAMNSSFEGVSGHVFDASGRMAWTLIEQLQGSYKKGITYDYS 438
QY 433 QLDNLSWLNTEQWI 446
Db 439 TKDDLSSWKTDKWI 452

RESULT 10
US-09-422-936-59
; Sequence 59, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
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; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-422-936-59

Query Match 27.6%; Score 1206; DB 4; Length 581;

Best Local Similarity 53.5%; Pred. No. 7.4e-114;

Matches 230; Conservative 73; Mismatches 105; Indels 22; Gaps 6;

QY 24 PHLOGGVAGRPDE----LHIGGIFPIAGKGGWGOACQACPAFRLALDDVYKQPNLLPGPK 79
Db 158 PHCQ--VSRTPHSERRAYIGALFPMSS--GGWPGGOACQAPVEMALEDYNRRDILPDYE 213
QY 80 LILHSNDECEPGLGASVYNNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIIVLCYGAS 139
Db 214 LKLIHDSKDPGQATKYLYELLYNDPIKILMPGSSSVTLVAEARMNLIIVLSYGS 273
QY 140 SPALSDRKRFPFLFTHPSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDLENRC 199
Db 274 SPALSNRQRFPTFFTHPSATLHNPTRVKLFKWKWKIATIQOTTEVFTSTLDDLEERV 333
QY 200 MEAGVEIVTROSFLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCEMYKQOLYGRAHVW 259
Db 334 KEAGIEITFRSFFSDPAPVKNLRQDARIIVGLFYETEARVCEVYKERLFGKKYVW 393
QY 260 FFIGWEDNWEVNLKABGICTCTVQMRIAARGHLTTALMNNQNTTISGMTAEERHRL 319
Db 394 FLIGWADNWFKT--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRISNMTSQEFVE 451
QY 320 RLNQALIEEGVDINHRYPE---GYOEAPLAYDAVMSVALAFNKMTWRLTTGKKSRLDFT 376
Db 452 KLTKRL-----KRHEETGGFQEAPLAYDAIWAALALANKTSGGSGRSGVRLEDN 502
QY 377 YDKEIADEIYAAMNSTOFLGSGVVAFFSSQGDRIALQIOMIDGKYEKLGYYDTQLDN 436
Db 503 YNNQITITDIYRAMNSSFEVSGHVHFDASGRMAWTLIEOLGGSYKKIGYDSTKDD 562
QY 437 LSWLNTQEWI 446
Db 563 LWSKTDKWI 572

RESULT 11

US-09-422-936-55
; Sequence 55, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55

; LENGTH: 578

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-422-936-55

Query Match

27.5%; Score 1205; DB 4; Length 578;

Best Local Similarity 53.3%; Pred. No. 9.3e-114;

Matches 228; Conservative 74; Mismatches 108; Indels 18; Gaps 5;

QY 24 PHLOGGVAGRPDE--LHIGGIFPIAGKGGWGOACQACPAFRLALDDVYKQPNLLPGFKLI 81
Db 155 PHCQVNRTPHSERRAYIGALFPMSS--GGWPGGOACQAPVEMALEDYNRRDILPDYELK 212
QY 82 LILHSNDECEPGLGASVYNNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIIVLCYGASSP 141
Db 213 LIHDSKDPGQATKYLYELLYNDPIKILMPGSSSVTLVAEARMNLIIVLSYSSSP 272
QY 142 ALSDRKRFPFLFTHPSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDLENRCME 201
Db 273 ALSNRQRFPTFFTHPSATLHNPTRVKLFKWKWKIATIQOTTEVFTSTLDDLEERVKE 332
QY 202 AGVEIVTROSFLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCEMYKQOLYGRAHVWF 261
Db 333 AGIEITFRSFFSDPAPVKNLRQDARIIVGLFYETEARVCEVYKERLFGKKYVWFL 392
QY 262 IGWEDNWEVNLKABGICTCTVQMRIAARGHLTTALMNNQNTTISGMTAEERHRL 321
Db 393 IGWADNWFKI--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRISNMTSQEFVEKL 450
QY 322 NQALIEEGVDINHRYPE---GYOEAPLAYDAVMSVALAFNKMTWRLTTGKKSRLDFTYT 378
Db 451 TKRL-----KRHEETGGFQEAPLAYDAIWAALALANKTSGGSGRSGVRLEDN 501
QY 379 DREIADEIYAAMNSTOFLGSGVVAFFSSQGDRIALQIOMIDGKYEKLGYYDTQLDNLS 438
Db 502 NOTITDIYRAMNSSFEVSGHVHFDASGRMAWTLIEOLGGSYKKIGYDSTKDDLS 561
QY 439 WLNTQEWI 446
Db 562 WSKTDKWI 569

RESULT 12

US-09-183-253-2
; Sequence 2, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:

[illegible]

Db 298 VSIPALNDSKYIGMSVYNVGIISCR1 323

Search completed: November 19, 2002, 10:51:40
Job time : 24 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 19, 2002, 10:51:09 ; Search time 11 Seconds
(without alignments)
1195.969 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGAVTWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues
Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2035	46.5	844	10	US-09-875-724-8
2	2032	46.5	844	9	US-09-793-139-55
3	2032	46.5	844	10	US-09-818-879-55
4	2032	46.5	844	10	US-09-211-755B-55
5	2032	46.5	844	10	US-09-875-724-6
6	2030.5	46.4	960	10	US-09-826-508-14
7	2029.5	46.4	793	10	US-09-875-724-4
8	2029.5	46.4	960	10	US-09-211-755B-56
9	2029.5	46.4	960	10	US-09-875-724-2
10	1290	29.5	941	9	US-09-793-139-47
11	1290	29.5	941	10	US-09-818-879-47
12	1290	29.5	941	10	US-09-211-755B-47
13	1284	29.4	898	9	US-09-793-139-2
14	1284	29.4	898	10	US-09-818-879-2
15	1284	29.4	898	10	US-09-211-755B-2
16	1283	29.3	940	10	US-09-818-879-4
17	1283	29.3	940	10	US-09-211-755B-4
18	1248.5	28.5	929	9	US-09-793-139-4
19	1158.5	26.5	874	10	US-09-826-508-26

20	697.5	15.9	332	10	US-09-826-508-28	Sequence 28, Appl
21	355	8.1	915	10	US-09-817-464-12	Sequence 12, Appl
22	355	8.1	922	10	US-09-817-464-14	Sequence 14, Appl
23	353	8.1	912	10	US-09-817-464-2	Sequence 2, Appl
24	321.5	7.4	867	10	US-09-817-464-4	Sequence 4, Appl
25	305	7.0	1203	12	US-10-027-923-5	Sequence 5, Appl
26	297.5	6.8	1212	12	US-10-027-923-4	Sequence 4, Appl
27	232.5	5.3	828	10	US-09-816-685-4	Sequence 4, Appl
28	227	5.2	1078	10	US-09-727-205-2	Sequence 2, Appl
29	219.5	5.0	1078	12	US-10-002-854-2	Sequence 2, Appl
30	205	4.7	839	9	US-09-897-427A-4	Sequence 4, Appl
31	199	4.5	843	12	US-10-124-598-2	Sequence 2, Appl
32	195	4.5	843	12	US-10-124-598-1	Sequence 1, Appl
33	194.5	4.4	852	10	US-09-796-338A-14	Sequence 14, Appl
34	192.5	4.4	604	10	US-09-820-809-13	Sequence 13, Appl
35	190.5	4.4	852	9	US-09-897-427A-6	Sequence 6, Appl
36	184	4.2	841	10	US-09-819-946-2	Sequence 2, Appl
37	180	4.1	841	9	US-09-897-427A-2	Sequence 2, Appl
38	178.5	4.1	763	10	US-09-819-946-4	Sequence 4, Appl
39	175	4.0	481	10	US-09-817-464-8	Sequence 8, Appl
40	172	3.9	926	10	US-09-816-685-2	Sequence 2, Appl
41	167.5	3.8	881	10	US-09-982-736-2	Sequence 2, Appl
42	166	3.8	669	12	US-10-124-598-7	Sequence 7, Appl
43	164	3.7	927	12	US-10-003-356-8	Sequence 8, Appl
44	162.5	3.7	464	10	US-09-796-338A-25	Sequence 25, Appl
45	162	3.7	1215	10	US-09-775-181-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-875-724-8
; Sequence 8, Application US/09875724
; Patent No. US20020091250A1
; GENERAL INFORMATION:
; APPLICANT: Kaupmann, Klemens
; APPLICANT: Bettler, Bernhard
; APPLICANT: Bittiger, Helmut
; APPLICANT: Frost, Wolfgang
; APPLICANT: Mickel, Stuart J
; TITLE OF INVENTION: Metabotropic GABA(B) Receptors, Receptor-specific
; FILE REFERENCE: 4-20876/A/PCT
; CURRENT APPLICATION NUMBER: US/09/875,724
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/194,382
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-724-8

Query Match	46.5%	Score	2035;	DB	10;	Length	844;
Best Local Similarity	49.3%;	Pred. No.	4e-172;				
Matches	387;	Conservative	151;	Mismatches	219;	Indels	28;
Gaps							9;
QY	23	SPHL--QGVAGRPDE----	LHIGIFFIAGKGGWGOACMPATRLALDDVNKPNLL	75			
Db	32	SPHLPRPHSRVPPHPSERRAVYIGALFWS--	GWPGGOACOPAVEMALEDVNSRDIL	89			
QY	76	PGFKLILHNSCEPCEGLASVYNNLYNKPQKMLLAGCSTVCTTVAEAKMNLIVLC	135				
Db	90	PDYELKLIHDSKDCPGQATKYLYELLYNDPIKILMPGSSVSTLVAEARMNLIVLS	149				
QY	136	YGASSPALSDRKRFPFLFTHPSATVHNPTRIKLMKFGWSVAIIQQAEVFISTVDL	195				
Db	150	YGSSSPALSNRQFPFFRTHPSATLHNPTRVKLFKWKWKIATIQQTTEFTSTLDDL	209				
QY	196	ENRCMEAGVEITVRSQFSLSDPTDAVNLRRQDAIIVGLFYVVAARVLCMEYKQOYLGR	255				

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Db 210 EERREAGIEITFROSFFSDPAPVKNLQRDARIIVGLFYETEARKEVCEVYKERLFGK 269
QY 256 AHWFEEFIGNYEDNWEVNLKAEIGITCVPMRIAABGHLLTTEALMNNQNTTISGMTAE 315
Db 270 KYVWELIGIYADNWFKI--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRISNNTSQ 327
QY 316 EFRHLNQLALIEEGYDINHRYPE---GYQEPAPLAYDAVWSVALANFNKMERLITTKKSL 372
Db 328 EFEVKLTREL-----KRHPEETGGFQEPAPLAYDAIWAALALNLTSGGGGRSGVRL 378
QY 373 RQFTYTDKEIADIEIYAAMNSTOPLGVSGVAFSSQGDRIALTQIEOMIDGKYEKLGYDT 432
Db 379 EDENYNNQITDQIYRAMNSSPFGVSHVFDASGRMAWTLIEQLGGSYKKGIDYS 438
QY 433 QLDNLISWLNTEQWIGKVPQDRITVTHVLTSLPLFVCMCTISSCGIFVAFALIIFNIW 492
Db 439 TKDDLWSKTDKWIIGSPADQTLVTKTRFELSOKLFISVSVLSLGLIVLAVCLSENIY 498
QY 493 NKHRRVYIQSHHPVCNTIMLFGVILICISVILLGIDGRFVSPPEYKICQARAWLLSTGFT 552
Db 499 NSHVRVYIQSNQPNLNLTAAGCSLAAVFPPLGIDGYHIGRNQFPFVQCARLWLLGLGFS 558
QY 553 LAYGAMFSKVRVHRETTK--AKTDPKPKVPEPKLYTMVSGLLSIDLVILLSHQIDPLQ 610
Db 559 LGYSGMFTKIWWVHTVTKKEEKEKWKTLPEPKLYATVGLLGMVDTLTAIWOIVDPLH 618
QY 611 RYLETFFPLEDPVSTDDIKIRPELEHCESSQNSMVLGLVYGFKGLIIVFGLFLAYETRSI 670
Db 619 RTIETFAKEPEKREDI--DVSILPQLEHCSKKNMTWLGIFYGKGLLLGIFLAYETKSV 677
QY 671 KYVQINDSRVYMSIYNNVVVLCITAPVGMVIAASQDASFAFVALAVIFCCFLSMILIFY 730
Db 678 STEKINDHRAVGMALYNVAVLCITAPVTMILSSQDAAAFASLAIVFSSYITLVVLFV 737
QY 731 PKVIEVIRHP--KDKAESYNPDASLSKDEERYQKLVTEQOLRLITQKEKIRVLQ 788
Db 738 PKMRLITRGWQEAQDTMTKGTSTNNNEEKSRLLEKENRELEKIIAEKERVSELH 797
QY 789 RLVER 793
Db 798 QLQSR 802

RESULT 2
US-09-793-139-55
; Sequence 55, Application US/09793139
; Patent No. US20020156265A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Kenneth A
; TITLE OF INVENTION: DNA Encoding A GABA BR2 Polypeptide And Uses Thereof
; FILE REFERENCE: 54002epctus
; CURRENT APPLICATION NUMBER: US/09/793,139
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Rattus Sp.
US-09-793-139-55

Query Match 46.5%; Score 2032; DB 9; Length 844;
Best Local Similarity 49.1%; Pred. No. 7.4e-172;
Matches 388; Conservative 151; Mismatches 213; Indels 38; Gaps 9;

QY 23 SPHLOGVAGRPD-----ELHIGGIFPIAGKGWQGGQACMPATRLALDDVVK 70
Db 32 SPHLP-----RPHVPYPHPSSERRAVYIGALFPMS--GGMVGGQACQPAVEMALDVNS 84
QY 71 QPNLLPGFKLILHNSDECEPGLGASVMYNLLYNKQKMLLAGCSTVCTVVAEAAKWN 130
Db 85 RRDILPDYELKLTHDSKCDPGQATKYLYELLYNDPIKIILMPGCSVSTLVAEAAKWN 144
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QY 131 LIVLYCASSPALSDRKRFPTLFRTHPSATVHNTRIKMKKFCWSRVAILLOQAEVFI 190
Db 145 LIVLYSGSSPALSNRQRFPTFFTHPSATLHNTRVKLFKFKWKKIATIQOTTEVFTS 204
QY 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVNLNRQDARIIVGLFYVVAARVLCENYKQ 250
Db 205 TLDDLERVKEAGIEITFROSFFSDPAPVKNLQRDARIIVGLFYETEARKEVCEVKE 264
QY 251 QLGRAHVWFEEFIGNYEDNWEVNLKAEIGITCVPMRIAABGHLLTTEALMNNQNTTIS 310
Db 265 RLFGKVVWELIGIYADNWFKT--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRIS 322
QY 311 GMTAEFRHLNQLALIEEGYDINHRYPE---GYQEPAPLAYDAVWSVALANFNKMERLIT 367
Db 323 NMTSQEVEVKLTREL-----KRHPEETGGFQEPAPLAYDAIWAALALNLTSGGGGR 373
QY 368 GKSLRDTYTDKEIADIEIYAAMNSTOPLGVSGVAFSSQGDRIALTQIEOMIDGKYEKL 427
Db 374 SGVLEDFNYYNNQITDQIYRAMNSSPFGVSHVFDASGRMAWTLIEQLGGSYKKI 433
QY 428 GYDTQLDNLISWLNTEQWIGKVPQDRITVTHVLTSLPLFVCMCTISSCGIFVAFALI 487
Db 434 GYDSTKDDLWSKTDKWIIGSPADQTLVTKTRFELSOKLFISVSVLSLGLIVLAVCL 493
QY 488 IFNIWNKHRRVYIQSHHPVCNTIMLFGVILICISVILLGIDGRFVSPPEYKICQARAWLL 547
Db 494 SFNIYNSHVRVYIQSNQPNLNLTAAGCSLAAVFPPLGIDGYHIGRNQFPFVQCARLWLL 553
QY 548 STGFTLAYGAMFSKVRVHRETTK--AKTDPKPKVPEPKLYTMVSGLLSIDLVILLSHQI 605
Db 554 GLGSLGYSGMFTKIWWVHTVTKKEEKEKWKTLPEPKLYATVGLLGMVDTLTAIWOI 613
QY 606 FDPQLRYLETFFPLEDPVSTDDIKIRPELEHCESSQNSMVLGLVYGFKGLIIVFGLFLAY 665
Db 614 VDPHRTIETFAKEPEKREDI--DVSILPQLEHCSKKNMTWLGIFYGKGLLLGIFLAY 672
QY 666 ETRSIKYVQINDSRVYMSIYNNVVVLCITAPVGMVIAASQDASFAFVALAVIFCCFLSM 725
Db 673 ETKSVSTEKINDHRAVGMALYNVAVLCITAPVTMILSSQDAAAFASLAIVFSSYITL 732
QY 726 LLIFVPKVIEWIRHPKDKAESK--YNPDASLSKDEERYQKLVTEQOLRLITQKEKI 783
Db 733 VLFVPPKMRRLITRGWQEAQDTMTKGTSTNNNEEKSRLLEKENRELEKIIAEKERV 792
QY 784 RVLRLVER 793
Db 793 SELRHQLQSR 802

RESULT 3
US-09-818-879-55
; Sequence 55, Application US/09818879
; Patent No. US20010023289A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Kenneth
; APPLICANT: Laz, Thomas
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA encoding a GABABR2 polypeptide and uses thereof
; FILE REFERENCE: 1795/54002DA
; CURRENT APPLICATION NUMBER: US/09/818,879
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/211,755
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(844)
```


[illegible]


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1      | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
Db    681   FTKLWVHTVFTRKEEKWKRTLEPMKLYATVGLLVGMDVLTAIWQIVDPLHRTIETF 740
       | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
QY     617   PLEDPVSTTODIKIRPELECHESQRSNMLGVGYFKGLILVFGFLAYETRSIKVKQLN 676
       | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
Db    741   AKEEPKEDI-DVSILPQLEHCSSRKNTWLGIIFYGYKGLLLLGIFLAYETKSVESTKIN 799
       | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
QY     677   DSRVVGMSIYNVVVLCITAPVGMVIASQQDASFAFVALAVIPCCFLSMILFIVPKVIEV 736
       | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
Db    800   DHRAVGMAIYNVAVLCITAPVTMILLSSQQDAAFASLAIVFPSSYITLVVLFVPKMRRL 859
       | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
QY     737   IRHP--KDKAESYNPDSATSKDEDERYQKLVKTENSQLORLITQKEEIRVLRQRULVER 793
       | : | : | | | | | | | | | : | : | : | : | | | | | | | | | | | |
Db    860   ITRGEWSEAQDTMKTGSTNNNEEEKSRLLKENRELEKIITAEKEERVSELRHQLQSR 918

RESULT 7
US-09-875-724-4
; Sequence 4, Application US/09875724
; Patent No. US20020091250A1
; GENERAL INFORMATION:
; APPLICANT: Kaupmann, Klemens
; APPLICANT: Bettler, Bernhard
; APPLICANT: Bittiger,, Helmut
; APPLICANT: Frost, Wolfgang
; APPLICANT: Mickel, Stuart J
; TITLE OF INVENTION: Metabotropic GABA[B] Receptors, Receptor-specific
; TITLE OF INVENTION: Ligands and their uses
; FILE REFERENCE: 4-20876/A/PCT
; CURRENT APPLICATION NUMBER: US/09/875,724
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/194,382
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 793
; TYPE: PRt
; ORGANISM: Homo sapiens
US-09-875-724-4
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Qy 454 RTIVTHVLRVTSLPLFVCMCTISSCGTFVAFALIIFNWKNHRRVQTQSSHPVCNTIMLPG 513
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 409 QTLWKTPRFLSQRLFIISVLSGLGVAVVCLSFNFIYNSHVRYIQNSQNLNNLTAVG 468
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 514 VIICLSIVILAGIDGRFVSPEYPKICOARAWLLSTGFTLAYGAMFSKVVRVHRETTK-- 571
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 459 CSLAALAAVFPGUGDGYHGIRNQFPFCOARUWLIGLGFSIGYSMFTKIWWHTVFTKKE 528
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 572 AKTDPKKKVKPWLKYTWVSGILLSIDLVLISWQIFDPLOQLRYLETFFPLEDPVSTDIDIKIR 631
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 529 EKKEWRTLEPWKLXYATVGLLVGDMLTALAIQIVDPLHRTIEFFAKEEPKEDI-DVSIL 587
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 632 PELECHESQRNSMWGLVGFKGILLVFGFLAYETRSIKVKQINDSRVVGMSIYNVVVL 691
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 588 POLECHCSRKMNTWLGIFYGKGLLLIGIFLAYETKSVESTEKINDHRAGMAIYNVAVL 647
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 692 CLITAPVGMVIASOODASFVALAVIFCCFLSMILLIFVPKVIEWIRHP--KDKAESKYN 749
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 648 CLITAPVTMIUSSOODAAFAPASLAIVFSSYITLVLFVPKMRRLITRGESOWEAOOTMK 707
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 750 PDSAISKDEDERYOKLVTENEQLORLIQTOKERIVRQRLVER 793
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 708 TGSSTNNEEKSRLLEKENKELEKIITAEREVSELRHQLSR 751
    :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

RESULT 8
US-09-211-755B-56
; Sequence 56, Application US/09211755B
; Patent No. US2002045742A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth A. Jones, Thomas M. Laz, Beth Borowsky
; TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And Uses Thereof
; FILE REFERENCE: 1795/54002-D
; CURRENT APPLICATION NUMBER: US/09/211,755B
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 09/186,664
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 960
; TYPE: prt
; ORGANISM: RAT;
US-09-211-755B-56
```

Query Match 46.48; Score 2029.5; DB 10; Length 793;
Best Local Similarity 49.98; Pred. No. 1.1e-171;
Matches 381; Conservative 151; Mismatches 211; Indels 21; Gaps 7;

QY	379	DKEIADBIYAMNSTOFLGVSGVVAFSSQGDRIALFOIEMIDGKYEKIYGYDQTOLDNIS	438
Db	501	NQITIDQIYRAMNSSSPGSGHWFTDAGSRMAWTLIEQLOGGSKYKIGYYDSTKDDLS	560
QY	439	WLNTEQWIGGKVPQDRITIVHVLRTVSLPLFVCMCTIISCGIFVAFALIFINWKNHRRV	498
Db	561	WSKTDKWIGGSPPADQTLVTKTFRFLSOKLFTISVSLSSIGIVLAVVCLSFNYSNHYRV	620
QY	499	IQSSHPCVNTIMLFGVITICILSVLLGIDGRFVSPPEYPKICOARAWLLSTGFTLAYGAM	558
Db	621	IQNSQPNLNLTAVGCSLAAAFVPLGLDGYHIGRSQFPVCOARLWLGLGFLSGYGS	680
QY	559	FSKVRVHREFTTK--AKTDPKKVPEWKLVTMYSGLLSIDVLVLSQWIFDPLQRYLETF	616
Db	681	FTKIWWVHTVFTTKEEKKEWKLTLEPWKLATVGLLVGMDVLTFLAIQVLDPLHRTIEF	740
QY	617	PLEDPVSTTDIIRKIPLECECSQRNMSWLGLVYFGKGLIFVGLFLAYETRSIKVKQIN	676
Db	741	AKEPKEDI-DVSTILPOLEHCKSKKNMTWLGIFYGYKGLLLGLIFLAYETKSVSTEKIN	799
QY	677	DSRYVGSIMYNNVVLCLITAPVGMVITASQODASFAVALAVIPCCFLSMLLIFVPKVIEW	736
Db	800	DHRVAGMAIYNVAVLCLITAPVTMLISSQODAAFAFASLAIVFPSSYITLWLVFPKMRL	859
QY	737	IRHPKDKAESK--YNPDSAIKSEDEERYQKLVITENEQLQRLITQKEKIRVLQRQLVER	793
Db	860	ITRGWQSETQDTMKTGSSTNNNEEEKSRLLKENRELEKIITAEKEERYSELRHQLQSR	918
RESULT 9			
US-09-875-724-2			
; Sequence 2, Application US/09875724			
; Patent No. US20020091250A1			
; GENERAL INFORMATION:			
; APPLICANT: Kaupmann, Klemens			
; APPLICANT: Bettler, Bernhard			
; APPLICANT: Bittiger, Helmut			
; APPLICANT: Frost, Wolfgang			
; APPLICANT: Mickel, Stuart J			
; TITLE OF INVENTION: Metabotropic GABA[B] Receptors, Receptor-specific			
; TITLE OF INVENTION: Ligands and their uses			
; FILE REFERENCE: 4-20876/A/PCT			
; CURRENT APPLICATION NUMBER: US/09/875,724			
; CURRENT FILING DATE: 2001-06-06			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/194,382			
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-25			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 960			
; TYPE: PRT			
; ORGANISM: Rattus norvegicus			
US-09-875-724-2			

[illegible]

Qy	262	IGWTEDNNWYVNLKAEGTCTCTVEQMRIAAEGLHTTEALMWNONNOTTISGMTAEERURL	321
Db	392	IGWADNNWFKT--YDPSINCTVEEMTEAVEGHTEIYVILMNPANPRISINMTSQBEVFKL	449
Qy	322	NOALIEEGYDINHDIRPE--GYOEAPLAYDAVWSVALAFNKTMERLITGKKSLRDFYTT	378
Db	450	TKRL-----KRHPETGGFQAPLAYDAIMALALANKTSGGGRSGVVRLEDFTN	500
Qy	379	DKEIADETIAAMNSTQFLGCVGVAFSSQGDRIALTQIEQIDMGKYERKLYGYDTOLDNLS	438
Db	501	NOTITDQIYRAMNSSFEVSGHVDFDASGRMAWTLIEQLGGGYSKKIYYDSTKDDL	560
Qy	439	WLNTEQWIGKVPQDRTIVTHVLRVSLPLFVCMCTTISCGIFAFAPALIIFNWNKHRRV	498
Db	561	WSKTDKWIQGGPPADQTVIKTFEFLSKFLTSVSLGSLGIVLAVVCLSFNIYNSHRY	620
Qy	499	IQSSHPVCNTMLFGVILICLSVILGIDGREFVPEEYPKICQARAWLLSTGFTLAYGAM	558
Db	621	IONSONPNNLTAVGCSALAAVPLGLDGHYGRSQPFVCOARLWLLGFGSLGYSGM	680
Qy	559	FSKVRVHRFTTK--AKTDPPKKVPEWPKLYTMVSGLLSIDLVILLSQWIFDPLQRYLETF	616
Db	681	FTKIMWHTVFTKKEKKEMWRTLEPWKLATVGLLVGMDVLTALWQIVDPLHRTIETF	740
Qy	617	PLEDPVSTTDIKIRPELHCHESQSNWGLVYCGFKGLILVFLGFLAYETPSIKVKQIN	676
Db	741	AKEEPKEDI-DVSHLPQLEHCHSCKNMTWLGIFYGYKGLLLGLIFLAYETKSVSTEKIN	799
Qy	677	DSRYVGSIMYNNVVLCLITAPVGMVIAQSQDAFPAFALAVIFCCFLSMLLIFVFPKVIEW	736
Db	800	DHRVGMALYNNVAVLCLITAPVTMLSSQDDAAFAFASIAVFSYITLVLFVFPKMRL	859
Qy	737	IRHPKDKAESK--YNPDSAIKEDERYOKLVTENEQQLRLTQKEEKIRVLRQRILVER	793
Db	860	ITRGWQSETQDTMTKGTSGSTNNNEEKSRLLEKENREKLEKIIAEKEERVSELRHQLQR	918
RESULT 10			
US-09-793-139-47			
; Sequence 47, Application US/09793139			
; Patent No. US20020156265A1			
; GENERAL INFORMATION:			
; APPLICANT: Jones, Kenneth A			
; TITLE OF INVENTION: DNA Encoding A GABA BR2 Polypeptide And Uses Thereof			
; FILE REFERENCE: 54002epctus			
; CURRENT APPLICATION NUMBER: US/09/793,139			
; CURRENT FILING DATE: 2001-02-26			
; NUMBER OF SEQ ID NOS: 55			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 47			
; LENGTH: 941			
; TYPE: PRT			
; ORGANISM: Homo Sapiens			
US-09-793-139-47			
Query Match 29.5%; Score 1290; DB 9; Length 941;			
Best Local Similarity 33.9%; Pred. No. 6.1e-108;			
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;			
Qy	18	LCLIASPHLOGGVACRP-----DELHTGGIPPI---AGKGWQGGQACMPATRLALDDV	68
Db	31	LLLPLAPGAWGARGAPRPPSSPPLSTMGMLPLKEVAKGSI--GRGVLPVLAELAEIQ	88
Qy	69	NKQPNLLPFGKLLILHNSDECEPGLGASVYNNLLYNKPKMLLAG-CSTVCTTVAEAAK	127
Db	89	RNESLLRPVF-LDLRLYDTECDNAGLKAFYDAIKYGPNNHLMVFGVCPVSTIIAESLQ	147
Qy	128	WNLNLVLCYGASSPALSBRKPPPTLFRTHPSATVINPFRILKMKFGWSRVAILOQAEV	187
Db	148	GNNVLQSFAAATTPVLADKKKYPYEFRTVPSDNAYNPAILLKLYQKRWGTLTQDVQR	207
Qy	188	FISTVEDLENRCWEAGVETVLTROSFLSPTDVAVRNI.RRODARITVGLFVVAARVVICFM	247

Db 716 RFQTNQKKEDSKTSTSVTSVNOASTSRLEGLQSEHRLRMKITELDKDLEEVTHQLOD 775
QY 793 RGDAGT-----ELMGATGVASAAVATTSPASLIN 823
Db 776 TPE-KTTVIKQNHQYQELNDILNLGNFTSTGGKAILKN 813

RESULT 14
US-09-818-879-2
; Sequence 2, Application US/09818879
; Patent No. US20010023289A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Kenneth
; APPLICANT: Laz, Thomas
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA encoding a GABABR2 polypeptide and uses thereof
; CURRENT APPLICATION NUMBER: US/09/818,879
; PRIOR FILING DATE: 2001-03-27
; PRIOR FILING DATE: US 09/211,755
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: human
US-09-818-879-2

Query Match 29.4%; Score 1284; DB 10; Length 898;
Best Local Similarity 34.2%; Pred. No. 1.9e-105;
Matches 280; Conservative 169; Mismatches 320; Indels 50; Gaps 17;

QY 37 LHIGGIPI---AGKGGWGGQACMPATRLALDDVKNQPNLLPGFKLILHSNDSCEPGL 93
Db 13 LSIMGLPLTKEVAKGSI--GRGVLPFAVELAIEQIRNESLLRPYF-LDLRLYDTECDNAK 69

QY 94 GASVYNLLYNKPKQLMLLAG-CSTVCTTVAEAAKWNLLIVLCYGASSPALSDDRKFPTL 152
Db 70 GLKAFYDAIKYGNHLMVFGGVCPSVTIIAESLOGNWLQVLSFAATTPVLADKKKYPYF 129

QY 153 FRTHPSATVHNPTRIKLMKFGWSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTROSF 212
Db 130 FRTVPDNAVNPAILKLLKHQYKRVGTLTQDVQRFSEVRNDLTGVLGYGEDIESTESF 189

QY 213 LSDPTDAVRNLRQDARIIVGLFYVVAARRVLCQYKQOLYGRAHVFFGTWEDNWE- 389
Db 310 KFH-----GY-----AYDGIWIAKTQRAMETHLHASSRHQIQDFNTDHTLGRILNA 359

QY 390 MNSTQFLGVSVAFSSQGDRIALTQIQMDIGKYEKLGYYDTQDNLNLSWLN-TEQWIGG 448
Db 360 MNETNFFGVTVQVFFRN-GERMGTIKFTQFQDSREVKVGEXNAVADTLEIINDTIRFQGS 418

QY 449 KVPQDRIVTHVTRVSLPLFCVMTISSCGIFVAFALIIFNWNKRRHVIOSSHPVCNT 508
Db 419 EPPKDKTIILEQLRKISLPLYSILSALTILGMIMASAFLEFFNKNRKNOKLIKMSPPYMN 478

QY 509 IMLFGVILCLSVLLGIDGFRVSPPEYKICQARAWLLSTGFTLAYGAMFSKVRVHRF 568
Db 479 LIILGGLMSYASIFLGLDGSFVSEKFPETICTVTRTILTVGYTTAFGAMFAKTRVRAI 538

QY 569 TTRAKTDPKKKVPEWPKLYTVMSGLSLDLVILLSNQIFDPQLQRYLETFFLE-DPYSTTDD 627
Db 539 FKNVKK-KKKIITKQKLLVIVGGMLLDILCLICQAVDPLRRRTVEKYSMEPDPAGR--D 595

QY 628 IKIRPELEHCESSORNSWILGYGFKGLILVFLGLAYETRSIKVKQINDSRVVGMSIYN 687
Db 596 ISIRPLEHECENTHMTIWLGIYVAYKGLMLFCFLAWETRNYSIPALNDSKYIGMSVYN 655

QY 688 VVVLCLITAPVGMVIAASQODASFAVALAVIFCCFSLMLLIFVPKVIETVRHP----- 740
Db 656 VGIMCIIGAASVFLTRDQPNVQFCIVALVIFCSTTILCLVFPKLTILTNFEDAQNR 715

QY 741 -----KDKAESKYNPD-SAIKSEDEERYQKLVTEQQLRLITQKEEKIRYLQRQLE 792
Db 716 RFQTNQKKEDSKTSTSVTSVNOASTSRLEGLQSEHRLRMKITELDKDLEEVTHQLOD 775

QY 793 RGDAGT-----ELMGATGVASAAVATTSPASLIN 823
Db 776 TPE-KTTVIKQNHQYQELNDILNLGNFTSTGGKAILKN 813

RESULT 15
US-09-211-755B-2
; Sequence 2, Application US/09211755B
; Patent No. US20020045742A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth A. Jones, Thomas M. Laz, Beth Borowsky
; TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And Uses Thereof
; FILE REFERENCE: 1795/54002-D
; CURRENT APPLICATION NUMBER: US/09/211,755B
; PRIOR FILING DATE: 1998-12-15
; PRIOR FILING DATE: 09/186,664
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: HUMAN;
US-09-211-755B-2

Query Match 29.4%; Score 1284; DB 10; Length 898;
Best Local Similarity 34.2%; Pred. No. 1.9e-105;
Matches 280; Conservative 169; Mismatches 320; Indels 50; Gaps 17;

QY 37 LHIGGIPI---AGKGGWGGQACMPATRLALDDVKNQPNLLPGFKLILHSNDSCEPGL 93
Db 13 LSIMGLPLTKEVAKGSI--GRGVLPFAVELAIEQIRNESLLRPYF-LDLRLYDTECDNAK 69

QY 94 GASVYNLLYNKPKQLMLLAG-CSTVCTTVAEAAKWNLLIVLCYGASSPALSDDRKFPTL 152
Db 70 GLKAFYDAIKYGNHLMVFGGVCPSVTIIAESLOGNWLQVLSFAATTPVLADKKKYPYF 129

QY 153 FRTHPSATVHNPTRIKLMKFGWSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTROSF 212
Db 130 FRTVPDNAVNPAILKLLKHQYKRVGTLTQDVQRFSEVRNDLTGVLGYGEDIESTESF 189

QY 213 LSDPTDAVRNLRQDARIIVGLFYVVAARRVLCQYKQOLYGRAHVFFGTWEDNWE- 271
Db 190 SNDPCTSVKLLGNDVRIILQGFQDNMAAKVFCAYEENMYGSKYQWIIPGWEPSSWEQ 249

QY 272 VNLKAEGITCTVEQMRIAAGHLLTTEALMWNQNNQTTISGMTAEERHRLNQALIEEGYD 331
Db 250 VHTEANSRCLRNKLLAAMEGYIGVDFEPLSSKQIKTISGKTPOQYEREYNNKRSRGVPS 309

QY 332 INHDYRPEGYQEAFLAYDAVWSVALAFNKTMERL--TTGKKSRLDFTYTDKEIADEIYAA 389
Db 310 KFH-----GY-----AYDGIWIAKTQRAMETHLHASSRHQIQDFNTDHTLGRILNA 359

QY 390 MNSTQFLGVSVAFSSQGDRIALTQIQMDIGKYEKLGYYDTQDNLNLSWLN-TEQWIGG 448
Db 360 MNETNFFGVTVQVFFRN-GERMGTIKFTQFQDSREVKVGEXNAVADTLEIINDTIRFQGS 418

QY 449 KVPQDRIVTHVTRVSLPLFCVMTISSCGIFVAFALIIFNWNKRRHVIOSSHPVCNT 508
Db 419 EPPKDKTIILEQLRKISLPLYSILSALTILGMIMASAFLEFFNKNRKNOKLIKMSPPYMN 478

[illegible]

Search completed: November 19, 2002, 10:52:13
Job time : 15 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	2024.5	46.3	960	2	JF0356	gamma-aminobutyric	
2	457	10.4	402	2	T29703	hypothetical prote	
3	356.5	8.2	912	2	JH0563	metabotropic gluta	
4	355	8.1	908	2	I49142	metabotropic gluta	
5	353	8.1	915	2	A49874	metabotropic gluta	
6	342	7.8	879	2	JG7160	metabotropic gluta	
7	334.5	7.6	871	2	A46742	metabotropic gluta	
8	333	7.6	879	2	JH0562	metabotropic gluta	
9	318	7.3	872	2	JH0561	metabotropic gluta	
10	303.5	6.9	1171	2	A42916	metabotropic gluta	
11	303	6.9	1218	2	S71376	glutamate receptor	
12	302.5	6.9	1180	2	JC2132	metabotropic gluta	
13	297.5	6.8	1212	2	JC2131	metabotropic gluta	
14	294	6.7	999	2	T27628	hypothetical prote	
15	268	6.1	1199	2	A41939	G protein-coupled	
16	232.5	5.3	976	2	T51137	ionotropic glutama	
17	219.5	5.0	1078	2	A36715	calcium receptor (
18	219	5.0	941	2	T51135	ligand-gated chann	
19	213.5	4.9	1088	2	B56713	calcium receptor (
20	212.5	4.9	1079	2	I59362	calcium/polyvalent	
21	212	4.8	1267	2	T21340	hypothetical prote	
22	211.5	4.8	925	2	T06128	hypothetical prote	
23	211.5	4.8	962	2	D86186	hypothetical prote	
24	201.5	4.6	912	2	T51131	ligand gated chann	
25	198.5	4.5	1085	2	S40476	Ca(2+)-sensing rec	
26	193.5	4.4	551	2	T30806	metabotropic gluta	
27	190.5	4.4	923	2	F84732	probable ligand-ga	
28	189.5	4.3	953	2	S84732	probable ligand-ga	
29	187	4.3	502	2	S69331	natriuretic peptid	

262 IGWYEDNWYEVNLKAEGITCTVEQMRIAAEGHLTTEALMWNQNNQTTISGMTAEFPHRL 321

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Db 392 IGVYADNWEKI--YDPSINCTVDEMEAVESGHTTEIVMLNPANTPNTSISNWTSEFVEKL 449
QY 322 NQALIEEGYDINHRYPE---GYQEPALYDAVMSVALAFNKTMRLETTGCKSLURDYTT 378
Db 450 TKRL-----KRPEETGGFQEPALYDAIWAALALANKTSGGGRSGVRLEDEYN 500
QY 379 DREIADEIYAAMNSTOFLGSGVAVSSQDRIALQIEQIDGKYEKLGYYDYDQLNLS 438
Db 501 NOTITDQIYRAMNSSSFGVGHVFDASGRMAWTLIEQPQGGSYKKIGYDSTKDDLS 560
QY 439 WLNTQEWIGKVPQDRFTIYTHVLTVSLPLFCVCMCTISSCGIFVAFALIIFNWKNHRRV 498
Db 561 WSKTDKWIIGSPADTLVTKTRFLSOKLFIISVLSLGGIVLAVVCLSFNINSHVRY 620
QY 499 IGSSHPVCNTIMLFGVILICLSVILGIDGRFVSPEEYPKICQARALLSTGFTLAYGAM 558
Db 621 IQNSOPNLNLTAVGCSLAAAVFPLGLDGYHIGRNQFPFVQCQARLLWLLGLGSLGYGSM 680
QY 559 FSKVWRVHR-FTTK-AKTDPKKKVPEWKLYTMVSGLLSIDLVILLWSQIDPLQRYLET 616
Db 681 FTKIMVWHTGFTKKEEKKERKLTLPWKLYATVGLLVGMDVLTALWQIVDPLHRTIET 740
QY 617 PLEDPVSTDDKIRPELEHESQORSNMLGLVYGFKGLLVFLGLFLAYETRSIKVKQIN 676
Db 741 AKEEPKEDI-DVSLPQLEHCSRKKNWTGLGIFYGKGLLLGIFLAYETKSVSTEKN 799
QY 677 DSRVYGMSTNVVVLITAPVGMVIAQQDASFALAVIFCCFLMLLIFFPKVIEV 736
Db 800 DHRVAGMAIYNVAVCLITAPVTMILSSQDAAFAFASLAIVFSSYITLVLVFVFKMRL 859
QY 737 IRHP--KDAESKYNPDSALSKEDEERYQKLTENEOQLRLITQKEKIRVLRORLVER 793
Db 860 ITRGEMQSEADTMKTGTSSNNNEEKSRLLEKENRELEKIIAEKERVSELRLHQLOS 918

RESULT 2
T29703
hypothetical protein ZK180.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T29703
R:Pauley, A.; Le, T. T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid ZK180.
A:Reference number: Z20669
A:Accession: T29703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <PAU>
A:Cross-references: EMBL:U58748; PIDN:AA852965.1; GSPDB:GN00022; CESP:ZK180.1
A:Experimental source: strain Bristol N2; clone ZK180
C:Genetics:
A:Gene: CESP:ZK180.1
A:Map position: 4
A:Introns: 25/3; 98/2; 219/3; 253/3; 280/1; 309/1; 339/2; 357/3; 395/2

Query Match 10.4%; Score 457; DB 2; Length 402;
Best Local Similarity 29.9%; Pred. No. 1e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 389 AMNSTOFLGSGVAVFSSQDRIALQIEQIDGKYEKLGYYDTQLDNLNLSNLT--TEQWI 446
Db 15 AIDNSSFOGLTGKVKFAN-NERGLVDIKQWSDQYVPFAYVDGADDEFKIIDSTTKGW- 72
QY 447 GSKVPQDRITVTHVLTSLPLFCVCMCTISSCGIFVAFALIIFNWKNHRRVIOSSHPVC 506
Db 73 --SPPLDSTITERREHISILFLAM-----SLF-----IKMSSPNL 107
QY 507 NTIMLFGVILICLSVILGIDGRFVSPEEYPKICQARALLSTGFTLAYGAMFSKVRVH 566
Db 108 NMIITAGSICTFASVIMGLDTRIVSPDFVWLCYTKTWTLCIGFTLSFGAMFSKTRVH 167
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QY 567 RFTTKAKTDPKKKVPWKLYTMVSGLLSIDLVILLWSQIDPLQRYLETFFLEDPVSTTD 626
Db 168 SIFTNIRM-D-RAAIRKDSKLIIFILGILLFIDICVLTVAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKIRPELEHESQORSNMLGLVYGFKGLLVFLGLFLAYETRSIKVKQINDSRVYGMSTY 686
Db 223 NIVTIPEKECKNSSGSGVFOAVLYAVKGLVILGCLFLAWETRHVNVPALNDSKIYIGTR-- 280
QY 687 NVVVLCLITAPVGMVIAQQDASFALAVLAVIFCCFL---SMLLIFVPKVIIEVIRHPDKR 743
Db 281 -----TGORDVQSREV-----FCHFLDDTNVVSRECAKDSKFSKTPNFI 319
QY 744 AESKYNPDSALSKEDE---ERYQKLTENEOQLRLITQKEKIRVLRORLVERGDAGKTE 800
Db 320 MKLFFN----FSKNSYGGFKNFQKLSFGFGFNIVFARSQVKKVKYIELARNPV-----GNE 369
QY 801 LNG-ATGVASRAVAVTISOPAS 820
Db 370 PRAYRRGLMKSVVAKTSOPMS 390

RESULT 3
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-Nov-2000
A:Accession: JH0563; I58149
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0563
A:Molecule type: mRNA
A:Residues: 1-912 <TAN>
A:Experimental source: brain
R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane,
Neuron 11, 41-52, 1993
A:Title: The ligand-binding domain in metabotropic glutamate receptors is related to
A:Reference number: I58149; MUID:93332699
A:Accession: I58149
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-123, 'R', 125-912 <RES>
A:Cross-references: GB:M90518; NID:g205400; PIDN:AAA93190.1; PID:g205401
C:Comment: This protein is coupled to a G protein and evokes a variety of functions b
C:Genetics:
A:Gene: GLUR4
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phos
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
F:588-610/Domain: transmembrane #status predicted <TRI>
F:625-645/Domain: transmembrane #status predicted <TRI>
F:657-675/Domain: transmembrane #status predicted <III>
F:700-720/Domain: transmembrane #status predicted <IV>
F:751-772/Domain: transmembrane #status predicted <TRV>
F:786-807/Domain: transmembrane #status predicted <TVI>
F:822-847/Domain: transmembrane #status predicted <VII>
F:98,301,454,484,569/Binding site: carboxylate (Asn) (covalent) #status predicted
F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 8.2%; Score 356.5; DB 2; Length 912;
Best Local Similarity 18.9%; Pred. No. 2.5e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

QY 5 MTSQDGAFTFW--IFLLCLIAS-----PHLQGVACRP-----DELHIGGIFPIAGK 48
Db 1 MSGKGGWAWWARLPLCLLLSLYAPVWPSSLGKPGKPHMNSIRIDGDTLGLGLFPVHGR 60
QY 49 GQWQGGQAC-----MPATRLALDDVKNQPNLLFGFKL----- 80
```


Db 870 IQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTTYISYSDHS 907

RESULT 5

A49874

metabotropic glutamate receptor 7 - rat

N:Alternate names: metabotropic glutamate receptor mGluR7

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

A:Accession: A49874; I57954

J:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, R. Biol. Chem. 269, 1231-1236, 1994

A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 cou

A:Reference number: A49874; MUID:94117433

A:Accession: A49874

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-915 <RES>

A:Cross-references: GB:D16817; NID:q458728; PIDN:BAA04092.1; PID:g458729

R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.

Mol. Pharmacol. 45, 367-372, 1994

A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid

A:Reference number: I57954; MUID:94195260

A:Accession: I57954

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-915 <RES2>

A:Cross-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658

C:Genetics:

A:Gene: MGLUR7

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: neurotransmitter receptor

Query Match 8.1%; Score 353; DB 2: Length 915;

Best Local Similarity 21.2%; Pred. No. 4.8e-19;

Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LCLIA-----SPH-----LAGGVAGRPDELHIGGIFPIAGKGGWGGQAC----- 57

Db 24 LLCVLAARAGQEWYAPHISRIEGDVT-----LGGFLFPVHAKG--PSGVPCGDIRREN 74

QY 58 ----MPATRLALDDVKNQPNLLPGFKL---IL----- 87

Db 75 GTHRLEAMLYALDQINSNDPNNLNTVLGARILDTCSRDTYALEQSLTFVQALIQKDSV 134

QY 88 ECEPGLGASVMYLLNKKPKMLLAGC--STVCTTVAEAAKMNLLVLCYGASSPALSD 145

Db 135 RCTNGEPP-----VFKPEKVGIVGASGSSVIMVANILRLFPQIPQISTASTAPELSD 188

QY 146 RKRFTLFRTHPSATVHNPTRIKMKFGWSRVAILQQAEEVFSTVEDLENRCMEAGVE 205

Db 189 DRYDFFSRVVPDPSQAQAVDIVRALGN-----YVSTLAS-EGSYGEKGE 236

QY 206 IVTRQSFSLDPTDAVNLR-----RQDA-----RIIVGLFVVAARRVLC-----EMYKOOL 252

Db 237 SFTQISKEAGGLCIAQSVRIPOERKQRTIDFDRIIKOLLDTPNRSRVVIFANDEDIKQIL 296

QY 253 YG--RA-HWFFFGIWDNW-----YEVNLAEGITCTVEQMRIAEG---HLTTEAL 299

Db 297 AAKRAQDQVGHFLWVGSDSGSKINPLQHEDIAEG-AITIQKRAVTEGFDAYFTSRTL 355

QY 300 -----MW-----NONNOTTISGMFAEEF-RHRLNQAALIEGVDINHDYRPEGYOEP 345

Db 356 ENNRNVWFAYEENFNCKLTISGSKEDTDKCTQERI--GKDSNYEQ--EG--KVQ 409

QY 346 LAYDAVMSVALAFNKTMRLETT-----GRKSLRDFTYTDKEIADETIYAAMNS 392

Db 410 EVIDAVYAMAHALHNMKLCADYRGVCPEMEQAGGKKLLKYIRHVN----- 456

QY 393 TQFLGVSQV--VAFSSQGDRIALQIOMIDGKYEKLYGYDTOLDNLSW-----L 440

Db 457 --PNSAGTPVPMKNGD-----APGRYDIFQYQTNTTNPGRYLIGQWTDLEQL 504

QY 441 NTE--QWIGG--KVPQ-----VSLPLFCVCMCTISSCGIFVAFALIIIFNIWNKHRR 459

Db 505 NIEDMONGKGVREIPSSVCTLPCKPGORKKTKGTPCCWTCPCDGYOYQDEMTCOHCP 564

QY 460 -----VLRT-----VSLPLFCVCMCTISSCGIFVAFALIIIFNIWNKHRR 497

Db 565 YDQRPNENRTCCQNPIPIKLEWHSFNAVIPVFLAMGLIAT-IFWMATFIYN-----DTP 619

QY 498 VIOSSHPCVNTIMLVGVIICILISVILGIDGRFVSPEEYKPKICQARAWLLSTGFTLAYGA 557

Db 620 IVRASGRELSVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRFVFLGCMGVIAA 672

QY 558 MFSKVRVHRTTAK---TDPKKKVEPKLYTWVSGLLSIDLVILLISWQIFDPLOQVLE 614

Db 673 LLTKNRIYRIFEQGKRSVTAP-RLISPTSLATISLLISVQLLGTVFWFGVDPNNIID 731

QY 615 TFPLEDPVSTDDIKIRPELCHESQSRNSMGLVYGFKGLILVFLGLAYETRSIKVKQ 674

Db 732 ----YDEHKTNNPQARGVLA-CDITDQIICSL--GYSILLMTCTVYAIKTRGVP-EN 783

QY 675 INDSRYVGMSTIYNNVVVLCITAPVGMVITASQODASFAPV-----ALAVIFCCFLSMLIF 729

Db 784 FNEAKPIGFTWYTCIVWLAFIPI--FPGTAQSAEKLVIQTTLTISNMLSASVALGMLY 841

QY 730 VPKVIEVIRHPKDKAESKYNPDPSAISKEDEERYOKLVTEENQOLQRLITQKEEKIRVLQR 789

Db 842 MPKYVYIIIFHPDELNVQKR-----KRSFRAVVTAAATMSSRLSHKPSDR----- 883

QY 790 LVERGDAGKTEL 801

Db 884 --PNGEAK-TEL 892

RESULT 6

JC7160

metabotropic glutamate receptor subtype 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

A:Accession: JC7160

R:Minoshima, T.; Nakanishi, S.

J. Biochem. 126, 889-896, 1999

A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype

A:Reference number: JC7160; MUID:20012997

A:Molecule type: DNA

A:Residues: 1-879 <MIN>

A:Cross-references: GB:AF170696

C:Genetics:

A:Gene: mGluR3

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane prot

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>

F:577-599/Domain: transmembrane #status predicted <TM1>

F:614-634/Domain: transmembrane #status predicted <TM2>

F:646-664/Domain: transmembrane #status predicted <TM3>

F:689-709/Domain: transmembrane #status predicted <TM4>

F:735-756/Domain: transmembrane #status predicted <TM5>

F:770-791/Domain: transmembrane #status predicted <TM6>

F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 7.8%; Score 342; DB 2: Length 879;

Best Local Similarity 20.5%; Pred. No. 3.2e-18;

Matches 182; Conservative 132; Mismatches 300; Indels 272; Gaps 41;

QY 36 ELHIGGIPPIAGKGGWGGQAC-----MPATRLALDDVKNQPNLLPGFKLLIHS 84

Db 38 DLVLGGLFPINEKG--TGTECRGINEDRGTRLEAMLFAIDENKNDVLLPGVKLVYHI 95

QY 85 NDS-----ECEPGLGASVMYLLNKKPKMLLAGC-- 115

Db 96 LDTCSRDTYALEQSLFVRASLTAKVDAEYMCPCD-----SYATQENIP-----LLIAGVIG 147

QY 116 ---STVCTTVAEAKMNNLIVLCYGASPSALSDRKRPTLFRTHPSAFVHNPTRIKLMKK 172

Db 148 GSYSSVSIQVALLRLFOIQISVASTSAKLSKSDRYDFARTVPPDFYQAKAMAILRY 207

QY 173 FGRSRVAILQAAEEVFISTVEDLE-----NRCMEAGVEIYTRQSFSLSDPTDAVRN-IJR 225

Db 208 FNTYVSTVASEGDTGTEAFQEAFLRNICIT-ATAEKVGRSNIRKSYDSVIRELLQK 266

QY 226 QDARIIVGLF-----YVVAARVLCEMYKQOLYGRAHWFEFGTWYEDNWEVNLKAE 277

Db 267 PNARVV-LFWRSDSRELIAASRV-----NASFTWV-----ASDQWG-----AQE 307

QY 278 GITCTVEQMRIAAGHULTTEAL-----MNQNNQTTIS 310

Db 308 SI---VKGSEHVAAGAITLELASHPVRFQDRYFQSLPNYNNHRNPFDFWEQKFCQSLQ 364

QY 311 GMTAEPRHLNQAIEEGYDINHIDRYPEGYQEAPLAY--DAVWSVALAFNKTWRL--- 365

Db 365 -----NKRNRHQICDKHLAIDSSNYE---QESKIMFVNAVYAMAHALHKMQRTLCPN 414

QY 366 TT-----GKSLRDFTYTDKEADELYAAMNSTQFLGSGVVAFFSSQGDRIALTQ 415

Db 415 TTCLDAMKILDKKKLYDKYL-----LKNFTAPFNPK--GADSIKVFDTYDGMGRYN 467

QY 416 I---EQMIDGKYE--KLGYDTQL-----DNLWLNTE----- 443

Db 468 VFNFQIHGGYSLYKVGHWAEYLDVDSIHWSSNSVPTSCSDPCAPNEMKNQPGDVC 527

QY 444 -----QW-----IGG--KVPQDRTIVTHVLR----- 462

Db 528 CWICICEPYEYLVDEFTCMDCGPGWPTADLSGCYNLPED-----YIRWEDAWAIGPV 581

QY 463 TVSLPLFVCMCTISSCGIFAFALIIENINWKNHR--VQSSHPVCNTIMLFGVIICLI 519

Db 582 TIACLGFMCTC-----IVTVFIKHNTPLVKASGRELC-YILLFGVSLSYC 627

QY 520 SVILLGIDGRFVSPEEYPKICOARAWLLSTGFTLAYGAMFSKVRVHREFTTKAKTDPK-- 577

Db 628 MTF-----FFTAKSPVICALRLRLGLGTSFAICYSALITKTNCIARIFDGVKNQAORP 680

QY 578 KKEVPKMLYPMVSGLLSIDVILLSMQIFDP--LQRYLETFFLEDVSTTDDIKIRPELE 635

Db 681 KFTSPSQVFICGLILVQVWVSWLILETPGTRRY--TLP-----EKRETVIL 728

QY 636 HCSQRNSMWGLVGFGLILVGLFLAYETRSIKVKQINDSRVGMYSIYVNVVLCIT 695

Db 729 KCVKDSMLISLYDY--VLVILCTVYAPKTRKCP-ENFNEAKFIGTMYTTTCIIWLAF 785

QY 696 APVGMVITASQODASAFVALAVIFCCFLSMILLIFVPKVIEWIRHPK 741

Db 786 LPFIYVTSYRQVTTTMCISVLSGFEVLGCLFAPKPVHVLFPQ 831

RESULT 7

A46742

metabotropic glutamate receptor, mGluR6 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C:Accession: A46742

R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 268, 11868-11873, 1993

A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m

A:Reference number: A46742; MUID:93280152

A:Accession: A46742

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-871 <NAK>

A:Cross-references: GB:D13963; NID:G391856; PIDN:BAA03066.1; PID:g391857

A:Experimental source: retina

A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:133250)

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 7.6%; Score 334.5; DB 2; Length 871;
Best Local Similarity 20.3%; Pred. No. 1.2e-17;
Matches 180; Conservative 158; Mismatches 350; Indels 199; Gaps 39;

QY 11 VTFWIF---LLCLIASPHLQGGVAGRPDBELHIGGIFPIAGKGGWQGCAC----- 57

Db 11 LAWLWSQAGIACGAGSVRLAGG-----LTGGGLFPVHARGA--AGRACGALKKEQGVH 61

QY 58 -MPATRLALDDVKNQPNLLPGFKLILHSNDSECE-----PGLGA 95

Db 62 RUEAMLYALDRYNADPELLPGVRLGARLLDT-CSDRTYALEQALSFEVQALIRGRGDGEA 120

QY 96 SV-----MYNLNKPOKLMLLAG--CSTVCTTVAEAKMNNLIVLCYGASPSALSDRKR 148

Db 121 SVRCGGVPPPLRSAPPERRVAVVGASASVSIMVANVLRFAIPQISYASTAPELSDSTR 180

QY 149 FPTLFRTHPSATVHNPTRIKLMKKGWSRVAIL-----QAAEEVFISTVEDLENRCME 201

Db 181 YDFFSRVVPPDSYQAQAWVDIVRALGNVYSTLASBGNYGESGVEAFVQISREAGGVCTA 240

QY 202 AGVEIVTRQSFSLSDPTDAVRNLR--ODARIIVGLFYVVAARRVLCEMYKQOLYGRAH 257

Db 241 QSIKIPREPCK---PGEFHKVIRRLMETPNARGIIIFANEDDIRRLEATRQANLTGH-- 294

QY 258 VWFYFGWYEDNWE-----VNLKAEGLTCTVEQMRIAAG---HLLTALMWNQNNQTT 308

Db 295 -FLWVG--SDSWGSKISPLNLEEEAVGAIITLPRKASIDGFDQYFMTLSL---ENNRN 348

QY 309 TSGMTAEPRHLNQAIEEGYD-----INHIDRYPEGYQEAPLAYDAVWSVA 355

Db 349 I--WFAEWEENFNCKLTSSGGQSDSTRTKCTGEERIGQDSAYEQEGKVFVIDAYATA 406

QY 356 LAFNKTMRLLTGGKSL-RDFTYTDKEIADEIYAAMNSTQFLGSGV-VAFSSQGD---R 410

Db 407 HALSHMQALCPGHTGLCPAMEPTD--GRTLLHYIRAVRFNGSAGTVPVFNENGDAPOK 463

QY 411 TALTOIE-----QMDGKYEKLYY--DTOLDNLWLNTEQWIGG--KVPQDRTIV----- 457

Db 464 YDIFOYQATNGSASSGGYQAVGQWAEALRLD---MEVLRWSGDPHEVPPSCSLPCGPG 519

QY 458 -----THVLR--TVSLPL 468

Db 520 ERKMKVGVPCWCHCEACDGYRFQVDEFTCEACPGDMRPTPHNCTGCRPTPVVRLTWSSPW 579

QY 469 FVCMCTISSCGIFAFALIIENINWKNHRVQSSHPVCNTIMLFGV-IICLSVILLGLD 527

Db 580 AALPELLAVLGIATTTIMATMRHNDTPIVRSGRELSVLLTGIFLIYAITFLMVA-- 637

QY 528 GRFVSPPEYPKICOARAWLLSTGFTLAYGAMFSKVRVHREFTTKAK--TDPKKKVEPWKL 585

Db 638 -----EPCAICAARLLILGTTLSYLSALLTKTNRIYRIFEQGKRSTVPPFISPTSQ 691

QY 586 YTMVSGLLSIDVILLSMQIFDPLQRYLETFFLEDVSTTDDIKIRPELEHESQSRNSMW 645

Db 692 LVITFGLTSLQVGVIAWLGAPPHSHVID----YEQRTVDEQARGVLR-CDMSDLSL- 745

QY 646 LGLVYGFGLIILVGLFLAYETRSIKVKQINDSRVGMYSIYVNVVLCITAPVGMVIAQ 705

Db 746 IGCL-GYSLILLMVTCTVVAIKARGVP-ETFEAKPKIGFTMYTTCIIWLAFVPI--FFGTA 801

QY 706 QDASFAFY-----ALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESK 747

Db 802 QSAEKIYIQTTLTVSLSLSASVSLGMLVYVPKTYVILPHPEQNVQKR 848

RESULT 8

JH0562

metabotropic glutamate receptor 3 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

C:Accession: JH0562
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TAN>

A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <SIG>
F:577-599/Domain: transmembrane #status predicted <TRI>
F:614-634/Domain: transmembrane #status predicted <TRI>
F:646-664/Domain: transmembrane #status predicted <TRI>
F:689-709/Domain: transmembrane #status predicted <TRI>
F:735-756/Domain: transmembrane #status predicted <TRI>
F:770-791/Domain: transmembrane #status predicted <TRI>
F:804-828/Domain: transmembrane #status predicted <TRI>
F:209,292,414,439/Binding site: carboxylate (Asn) (covalent) #status predicted <VII>
F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.6%; Score 333; DB 2; Length 879;
Best Local Similarity 20.6%; Pred. No. 1.6e-17;
Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

QY 36 ELHIGGIPIACKGGWGGQAC-----MPATRLALDDVKNQPNLLPGFKLILHS 84
DB 38 DLVLGGLFPINEKG---TGPEECGRINEDRGIOKLEAMLFADINDKNLVLPGVKLGVIH 95
QY 85 NDS-----ECEPGLGASVMVNLNKKPKMLLAGC-- 115
DB 96 LDTCSRDTVALQSLFEFVRASLTKVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147
QY 116 ---SVTCVTVAAKMWNLIVLCYGASSPALSDDKRPFLRPHSPATVHNPTRIKLMKK 172
DB 148 GSYSSVSIQVALLRFQIPQISYASTSAKLSKSDYDFARTVPDPYQAKAMAEILRF 207
QY 173 FCMRSVAILQAAEEVFISVEDE-----NRCMEAGVELVTRQSLDPTDAVRN-LRR 225
DB 208 FNTVTVSTVASGDEYGETGIEAFQEARLNICI-ATAEKVGRSNTRKSYDSVIRELLQK 266
QY 226 QDARIIVGLF-----YVVAARRVLCEMYKOOLOGYRAHVWFEGWYEDNMYEVNLKAE 277
DB 267 PNARVVV-LFMRSDDSRELIANRV-----NASFTWV---ASDCWG-----AQE 307
QY 278 GITCTVEQMRIAAGHLTTEAL-----MWNQNNQTTIS 310
DB 308 SI---VKGSEHVAYGAITLASHVPVQFDYFQSLNPNYNNHRNPFRDFWEQFQCSLQ 364
QY 311 GMTAEFRHLNQAILEEGYDINHDPYQGYQAPLAY--DAVSVALAPNKWTHERLTTG 368
DB 365 -----NKRNRHQCDKHLADSSNYE---QESKTFMVVNAVYAMAHKMQRTLCPN 414
QY 369 KKSRLDF--TYTDKEIADSIYAAVNSQFL---GYSVVVAFSSQGDRIALTQI--EOMI 420
DB 415 TTKLCDAMKILQKLYKYLKINFTAPFNPNKGADSIKFTFTDGGHRYVNFNLQQT 474
QY 421 DGKYE--KLGYY-----DTQDLNLSW---LNTQ-----WI----- 446
DB 475 GCKYSLVKVGHWAETLSLDVDSIHWRSNVSPTSQCSDDPCAPNEMKNQPGDVCWCICIPC 534
QY 447 -----GGKVP-----QDRTTVTHVTRVSLPLFCVCMC 473
DB 535 EPEYVLVDEFTCDGCPGOWPTADLSGCYNLPEDYIKWEDAWAIGPV--TIACLGFLCTC 592
QY 474 TISSCGIFAFALIFINWKNRR---VIOSSHPVCNTMLFGVVICLISVILLGIDGRF 530
DB 593 -----IVTVTFIKHNTPLVRASGRELC-YILLFGVSLSYCMTF-----F 631

QY 531 VSPEEYKICQARAWLLSTGFTLAYGAMFSKWVRHRETTKAKTDPK--KKVEPKLYTM 588
DB 632 FIAKSPVICALRRGLGTSFAICYALLRTNCIRIDFGVKNGAQRKPFISPSQVFI 691
QY 589 VSGLLSIDLVLILLSQWIFDP--LQRYLETFFLEDVPVSTDDIKIRPELEHCESSNMSWL 646
DB 692 CLGLILVQIVMVSWMILLETPTGPRY--TLP-----EKRETVILKCNVDSSMLI 739
QY 647 GLVYFGKGLILVFLGLFLAYETRSIKVKOINDSRVYVMSIYNVVVLCITAPVGMVIAQQ 706
DB 740 SLTYDV--VLVILCTVYAFKTRKCP-ENFNEAKFIGHTYTTCTIWLAFLEFVYVTSDDY 796
QY 707 DASFAFVALAVICCFLLSMILLIFVPKVIETVIRHPK 741
DB 797 RVQTTTMCISVLSLGGFVVLGCLFAPKVIHLVFPQ 831

RESULT 9

JH0561
metabotropic glutamate receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
C:Accession: JH0561
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0561
A:Molecule type: mRNA
A:Residues: 1-872 <TAN>

A:Experimental source: brain

C:Comment: This protein is coupled to a G protein and evokes a variety of functions b

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>

F:568-590/Domain: transmembrane #status predicted <TRI>

F:605-625/Domain: transmembrane #status predicted <TRI>

F:637-655/Domain: transmembrane #status predicted <TRI>

F:680-700/Domain: transmembrane #status predicted <TRI>

F:726-747/Domain: transmembrane #status predicted <TRI>

F:761-782/Domain: transmembrane #status predicted <TRI>

F:795-819/Domain: transmembrane #status predicted <TRI>

F:308,386,402,547/Binding site: carboxylate (Asn) (covalent) #status predicted

F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted

F:832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.3%; Score 318; DB 2; Length 872;
Best Local Similarity 19.7%; Pred. No. 2.4e-16;
Matches 181; Conservative 135; Mismatches 330; Indels 274; Gaps 38;

QY 17 LLCLIASPHLOGGVAGRP-----DELHIGGIFFPIAGKGGWGGQACMP----- 59
DB 4 LLGLFALLLLMGVAEGPAPKVLFLGDLVLGGLFPVHQKGG--PAEECPGVNHRGTQR 61
QY 60 --ATRLADDDVKNQPNLLPGFKLILHSNDS-----EC 89
DB 62 LEAMFLALDRINRDPHLLPGVRLGALHILDSCKDTHALEQALDFVRASLRGADGSRHIC 121
QY 90 EPGLGASVMVNLNKKPKMLLAG--CSTVCTTVAAKMWNLIVLCYGASSPALSDDK 147
DB 122 PDG-----SYATHSDAPTAVTGVIGSYSDVSIQVALLRFQIPQISYASTSAKLSKDS 176
QY 148 RFPFLRTHPSATVHNPTRIKLMKKFGHSRVAIL-----QQAEEVFIS 190
DB 177 RYDYFARTVPDPFFQAKAMAEILFRFNNTYVSTVASGDEYGETGIEAFELFARARNICVA 236
QY 191 TVELENRCMEAGVEIVTROSFLSDPTDAVRN--RRDARIIVGLFVVAARRVLCEMY 248
DB 237 TSEKVGAMSRAPAEQGVVR-ALLOKPSARVAVLTRSDAREL-----LATQRL----- 285
QY 249 KQOLYGRAHVWFFIGWYEDNMYEVNLKAEGITCTVEQMRIAAGHLTTEALM----- 300

Db 286 -----NASFTW-----ASDGHGAL-----ESVAGSER-----RAEGAITIELASYPISDFRAS 329
QY 301 -----WNQNOTTISGMTAEER-----HRLNQALIEGYDINHRYPEGYQE 343
Db 330 YFQSLDPWNSNRNPFREFEERHCSFRQDCAHSLRAVPFE-----QE 375
QY 344 APLAY-----DAVWSVALAFNKMTMERL-----TTGKSLRDFYTDK-----380
Db 376 SKIMFVNAVYAMAHALHNMHRALCPNTHLCDAMPVNGRRLYKDFVLNKFDAFPERPA 435
QY 381 EIADEIYAAMNSTOFLGSGVVAESSQDRIALTQIEQIDG-----AYEKLGY-----430
Db 436 DTDDE-----VREDFGDIGRYNIFTYLRAGSGRYQKVGWAEGLT 479
QY 431 -DTQDNLWSLNTQEWIGGKVPQDR-----TIVTHVLRVSLPLFVC-----MC-----473
Db 480 LDTSF-----IPWASPS-----AGPLPASRCSEPCLONEVKSQV-----PGEVCCWLCIPQCPYEYRLD 533
QY 474 -TISCGI-----FVAF-----ALIFINWKNHR 496
Db 534 EFTCADCGLYGWPNASLTGCFELPQEIYRWGDAMAVGPVTIACIGALATFLVLGVFVRHN 593
QY 497 R-VIQSHHPVCNTIMLFGVILISVILLGIDGRFVSPEYKPKICQARAWLLSTGFTLA 554
Db 594 ATPVVKASGRELCYILGGVFLCYCMTFV-----FIA-KPSTAVCTLRRLGLGTAFSVC 646
QY 555 YGAMESVVRVHRFTTAKTDPKKK-----VEPWKLYTMVSGLLSIDLAVILLSQWIFDPLQRY 612
Db 647 YSALLTNTNRIARFEGAREGAQRPFISPASQVAICLALISGQLLIVAAMLVBEAPGTG 706
QY 613 LETFPLEDPVSTDDIKIRPELEHCESSQNSMWLGLVYGFGLIIVLFGFLAYETRSIKV 672
Db 707 KETAPERREVTL-----RCNHRDASMLGSLAVN-----LLIALCTLYAFKTKCP- 753
QY 673 KQINDSYVGMISYVNVVLCLITAPGVMIASQDASFAFVALAYIFCCFLSMLLIFVPK 732
Db 754 ENFNEARFICFTMTYTTCIILWALPIFYVTSDDRYVQTTMCVSVSLSGSVVLGCLFAPK 813
QY 733 VIEVIRHPDKAESKYNPDS 752
Db 814 LHILFQPKNVVSHRAPTS 833

RESULT 10

A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A42916
R:Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5
A:Reference number: A42916; MUID:92317054
A:Accession: A42916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <ABE>
A:Cross-references: GB:DI0891; NID:g220813; PIDN:BAA01711.1; PID:d1002186; PID:g220814
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBI:P107750)
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 6.9%; Score 303.5; DB 2; Length 1171;
Best Local Similarity 19.9%; Pred. No. 5.1e-15;
Matches 203; Conservative 144; Mismatches 387; Indels 287; Gaps 43;

QY 30 VAGRPDELHGTGIPPI-----AGKGWQGGQACMPATRLALDDVKNQPNLLP 76
Db 28 VAHMPGDIIIGALFSVHHQPTVDKVKHCKGAVREQYGIORVEAMLHTLERINSPTLLP 87
QY 77 GFKLILHSND-----SECEPCL-----GASVWYNLLYNKPKQL 109

Db 88 NITLGEIRDSCWHSVALEQSIETIRDSLSIEEEGLVRCVDGSS-----SFRSKKPIVG 144
QY 110 MLIAGSCTVCTTVAEAAKMNWNLVLCYGASSPALSQRKRPPTLFRTHPSATVHNPRIKL 169
Db 145 VIGPGSSVAIQVONLQLLENIPQIAYSATISMDLSKTLFKYFMRVVPDQAQARAWDI 204
QY 170 MKKFGNSRVAILOOAAEEVFISTVEDLENRCMEAGVEIVTRQSFLSDPTD-----AVNRLR 224
Db 205 VKRYNNTYVSAVTEGNYGESGMEAFKDSAKEGICITAHYSKYISNAGEOSFKLLKLR 264
QY 225 RQ---DARIIVGLFVYVAARVLCENKQOYLGRAHWFFIGWYEDNW---YEV-----NL 274
Db 265 SHLPKARVACFCEGTVRGLLMAMRRLGLAGE-----FLLGSDGMADRYDVTGYQRE 319
QY 275 KAEGICTVTEQ-----MRIAEGHLLTEAL---MWNQNOTTISGMTAB---EFRHR 320
Db 320 AVGGITIKQSPDKVDFDDYYLKLREPETNLRNPFQFQHRFOCRLEGAQENSYNKT 379
QY 321 LNQALIEGYDINHRYPEGYQEAFLAY---DAYWSVALAFNKMTMERLTTGKSLRDFTYT 378
Db 380 CNSSLTLRTHV-----QDSKMGFVINAISYMAYLHNMQMSLCPGYAGLCD---A 427
QY 379 DKEI-ADIEIYAAMNSTOFLGVSG-VVAFSSQGDRIALTQIEQIDGKYELGYDQTDN 436
Db 428 MKPIDGRKLLDSLMKNTFTGVSGDMILFDENGDS-----PGRYEIMNEKMGKDY 477
QY 437 LSWLNTQEWIGGKVPQDRITV---THVLRV-SLPL-----468
Db 478 FDIYINGVNDGELKMDDEWNSKNNIIRSCVSECEKQIKVIRKGEVSCCWTCTPK 537
QY 469 -----FVC-MCTISS-----CGIF-----VAFAL 486
Db 538 ENEYVEDEYTCACQLGSWPTDGLTCDLIPVOYLWGDPEPIAAVVFACGLLALFVT 597
QY 487 IIFNIWKNHRRVIOSSHHPVCNTIMLFGVII-----CLISVILLGIDGRFVSPEYKPKIC 540
Db 598 VIFIIVRDTVPVKSSSREL-C-YIILAGICLGYLCTFLCIA-----KPK-- 639
QY 541 QARAWLLSTG-----TLAYAMESKVRVHRFTTAKTDPKKVEPWKLYTMVSGLLSID 596
Db 640 QIYCYLQIRIGISLPAMSYSALVTKTNRIARILAGS-----KKICTKPRFMSACQOLVI 695
QY 597 LVILLWSQIFDPLQRYLETFFLEDPVSTDDIKIRPELEHCESSQNSMWLGLV---YGFKG 654
Db 696 AFILICIQ-----LGIIVALEIMEPPDIMHDYPSIREVYLIC-----NTNLGVVTPLYNG 747
QY 655 LILVGLFLAYETRSIKVKQINDSYVGMISYVNVVLCLITAPGVMIASQDASFAFVA 714
Db 748 LLILSCTFFYAFKTRNVP-A-NFNEAKVIAFTMYTTCIILWALFVPI-----YFGSN 795
QY 715 LAVIFCCF-----LSMLLIFVPKVIEWIRHPDKAESKYNPDSAI-----SKEDE 759
Db 796 YKIITMCFVSLSATVALGCMFVPKVIILAKPERNVRSAFTTSTVVRMHVGDGSSAA 855
QY 760 ERYQKLV-----TENEQ-----LQRL---ITOKEK-----782
Db 856 SRSSLSLVNLWKRSGSGETLSSNGKSVTWAQNEKSTRGOHLWORLDVSHINKENPNQAV 915
QY 783 IRLVRLRVERGD---AKGTENLNGATGVASAAVATTSSQASLINSSAHATPAATLITOG 839
Db 916 IXPFPKSTENRPGGAAGGSGPGVAGAGNAGCTATGCP-----EPDAGPKALYDVAEA 970
QY 840 E 840
Db 971 E 971

RESULT 11

S71376
glutamate receptor homolog - cherry salmon
C:Species: Oncorhynchus masou (cherry salmon)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-May-1998

[illegible]

Db 668 YQRLLVGLSATMICYSALVTYKTNRIARILAGSKKKICTKRPKPMASAWAQIIVTAGLLVSQV 721

Qy 597 LVILLWSQIFDPLQRYLETFFLEDVSTDDIKIRPELEHCEQSQRMSMLGLV--YGFKG 654

Db 728 LTLEVTLLLEP-----PM-----PVKSYSPSIREVFLICNTSVGMVAPLGYNG 771

Qy 655 LILVFGFLAYETRSIKVKQINOSRYVGMISYVNVVLCITAPVGM-----VIASOODAS 709

Db 772 LLIMSVTYAPKTRNVA-NFNEAKYIAFTWYTTCTIIWLAFAVPIYFGSNYKIITT-----S 826

Qy 710 FAFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESKYNPDAS1 754

Db 827 FS-VLSVST-----VALGCMFSPKIYIILAKPERNVRSAFTTSDV 866

RESULT 12

JC2132

metabotropic glutamate receptor 5 A - human

C:Species: Homo sapiens (man)

C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1999

R:Accession: JC2132

R:Minakami, R.; Satsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.

Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994

A:Title: Molecular cloning and the functional expression of two isoforms of

A:Reference number: JC2131; MUID:94197696

A:Accession: JC2132

A:Molecule type: mRNA

A:Residues: 1-1180 <MIN>

C:Comment: This protein is coupled to guanine nucleotide binding proteins.

C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein

F:580-604/Domain: transmembrane #status predicted <TM1>

F:617-637/Domain: transmembrane #status predicted <TM2>

F:644-664/Domain: transmembrane #status predicted <TM3>

F:694-714/Domain: transmembrane #status predicted <TM4>

F:738-759/Domain: transmembrane #status predicted <TM5>

F:773-794/Domain: transmembrane #status predicted <TM6>

F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 6.9% Score 302.5; DB 2; Length 1180;

Best Local Similarity 20.1%; Pred. No. 6.1e-15;

Matches 208; Conservative 141; Mismatches 375; Indels 311; Gaps

Qy 30 VAGRPDELHIGGIPI-----*AGKGWQGGQACMPATRLALDDVNKQPNLLP 76

Db 28 VAHMPGDIIGALFSVHHQPTVDVHERKCGAVREQYGIQRVEAMLTLERINSDPTLLP 87

Qy 77 GFKLILHSD-----SCEPGL-----GASVMTNLYNKPQKL 109

Db 88 NITLGCETRDCWHSVALEQSIIEFRDLSITSEEEGLVRCVDGSSSPR--SKRPVIG 145

Qy 110 MLLAGCSVCTTVAEAAKMWNLIVLCYGASSPALSDDRKEPTLFRTHPSATVHNPTRIKL 169

Db 146 VIGPGSSVAIQVNLQLFNPQIAYSAISMDSDKTLFKYPMRVVPSDAQARAMVDI 205

Qy 170 MKKFCWSRVAILQQAEEVFISTVDLENRCMEAGVEIVTRQSFSLDPTD-----AVRNLR 224

Db 206 VKRYNWTYSAVHTEGNYGESMEAFKMSAKEGICIAHSYKIYSNAGEQSPDKLLKLT 265

Qy 225 RQ--DARLIIVGLFYVAARRVLCEMYKOOLYGRAHWFFIQTWEDNW---YEV-----NL 274

Db 266 SHLPARTVAVACFCEGTVRGLLMARRLGLAGE-----FLLIGSDGWADRYDVTGQYRE 320

Qy 275 KAGTICTVEQ-----*MRTAAEGLTTEALMKNONNOTTISGMTAEFEFRHLNQA 324

Db 321 AVGGTITIKLQSPDKVWFDDYVYKLRLPE---TNHRNPMFQ-----EFQHRFQCR 366

Qy 325 LIEEGYDINHORY-----PEGYQEAFLY--DAVMSVALAFNKTMERLTTGKKS 371

Db 367 L--EGFPQENSKYKNTCSNLTTLTHHVQDSKMGFVINAIYSWAYGLHNMQMSLCPGYAG 424

Qy 372 LRDTFTYTKET-ADFIYAAMNSTQFLGVG--VVAFFSQGQRIALQTQEQMDIGKYEKLYG 429

Db 425 LCD---AMKPIDGRKLLLESMTNFTGSGDTILFDENGDS-----PCRYEIMNF 471
QY 430 YDOLDNLSWLNTEQWIGGKVPQDRIV---THVLRTV-SLPL----- 468
Db 472 KEMGKDYFDYINVGSWDNGELKMDDEWVSKSNIRSVCSPECKGQIKVIRKGEVSC 531
QY 469 -----FVC-MCTISS-----CGIF----- 481
Db 532 WTCPCKENEYVDEYTCACQGLGSWPTDGLTGVYLIRWGDPEPIAAVVFACGLG 591
QY 482 --VAFALIFNWKHRRVIOSSHPVCNTIMLFGVII-----CLISVILLGIDGRFVSP 533
Db 592 LATLFVTVFIIYRDPVVKSSREL-C-YIILAGICLGLVCTFCLIA----- 637
QY 534 EEPKICQARAWLLSTGF---TLAYGAMFSKVMRVHRTTAKTDPRKKKVPKLYTMV 589
Db 638 --KPK--QIYCYLQRIQIGLSPAMSYSAVTKTNRIARLAGS-----KKKICTKKPRFMS 689
QY 590 SGLLSIDLVLISWQIFDPLQRYLETFFLEDPVSTDDIKIRPELEHESQSRNSMWGLV 649
Db 690 ACAQLVIAFLICIQ---LGIIVALFIMEPPDMDHYPISREVYLIC---NTNLGVV 741
QY 650 --YGFKGLILVFLGLFLAYETRSIKVKQINDSRVYVGMYSYNNVVLCLITAPVGMVIAQQD 707
Db 742 TPLGYNGLLILSCTFYAFKTRNPA-NFNEAKYIAFTMTTCIIWLAFVPI----- 791
QY 708 ASFAFVALAVIFCCF-----LSMLLIFVPKVIIVIRHPDKAKSKYNPDSAI----- 754
Db 792 --YFGSNYKIITMCFVSLSATVALGCMFVKYIILAKPERNVSATTTSTVVRMHVGD 849
QY 755 --SKDEERYOKLV-----TENEQ-----LQRL-----ITOKE 780
Db 850 GKSSSAASRSSSLNLMKRRGSSGETLRNGSKVSTWQAQNEKSSRGHLWQLSIHINKKE 909
QY 781 EKIRVLQRVLVERGDAKTENL-----CATGVASAAVATTSOPASLINS 825
Db 910 NP-----NQTAVIKFPFKSTESGLGPRGAGGAGGAGGAGGAGGPGP-----ES 960
QY 826 AHATPAATLAITQGE 840
Db 961 PDAGPKALYDAEAE 975

RESULT 13

JC2131
metabotropic glutamate receptor 5 B - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2131
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131; MUID:94197696
A:Accession: JC2131
A:Molecule type: mRNA
A:Residues: 1-1212 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F:560-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 6.88; Score 297.5; DB 2; Length 1212;
Best Local Similarity 20.08; Pred. No. 1.6e-14;
Matches 194; Conservative 141; Mismatches 360; Indels 275; Gaps 41;
QY 30 VAGRPDELHIGGIPPI-----AGKGGQGGQACMPATRLALDDVKNOPNLLP 76
||| : : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : |||

RESULT 14

T27628
hypotheical protein 2c506.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T27628

Db 28 VAHMPGDIIIGALPSVHHQFTVDKVKHRCQAVREQYGIORVEMLHLTERINSDDPTLLP 87
QY 77 GFKLILHSND-----SECEPL-----GASVMYNLLYNKPQKL 109
Db 88 NITLGEIRDSCHWSAVALQSISTEIRDSLISSEEEGLVRCVDGSSSFR--SKRPVIG 145
QY 110 MLLAGSTVCTTVAEAAKMNVLIVCYGASSPALSDRRPPTLFRTHPSATVINPPIKIL 169
Db 146 VIGPGSSVAIQVONLIQLFNIPQIAYSATSMDSLSDTKLFKFMVVPVPSDAQARAMVDI 205
QY 170 MKKFGSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTQSFSLSDPTD-----AVENLR 224
Db 206 VKRYNNTYVSATFEGNYGESMEAFKMSAKEGICIAHSYKIYSNAGSEQDFKLKKLKT 265
QY 225 RQ--DARIIVGLFVYVAARRVLCMKQOQLYGRAHVFFIGWEDNW---YEV-----NL 274
Db 266 SHLPKARVACFEGMTVRGLLMMARLGLAGE-----FLLGSDGWADRYDVTGYORE 320
QY 275 KAEGITCTVEQ-----MRIAAGHLTTEALMNNQNNOTTISGMTAEERFHRNLQA 324
Db 321 AVGGITIKLQSPDVKWFDDYYLKLPE---TNHRNPWFQ-----EFQHRFRQCR 366
QY 325 LIEEGVDINHRY-----PEGYQAPLAY--DAVSVVALAFNKTMERLTTGKKS 371
Db 367 L--EGFPQENSKNKTCNSSLTLKTHHVQDSKMGFVINAIIYSMAYGLHNMQMSILCPGYAG 424
QY 372 LRDFTYTDKEI-ADEIYAAAMNSQFELGVSG-VVAFSSQGDRIALTQIEQMDCKYKELGY 429
Db 425 LCD---AMKPIDGRKLLLESMTNFTGSGDTILFDENGDS-----PCRYEIMNF 471
QY 430 YDOLDNLSWLNTEQWIGGKVPQDRIV---THVLRTV-SLPL----- 468
Db 472 KEMGKDYFDYINVGSWDNGELKMDDEWVSKSNIRSVCSPECKGQIKVIRKGEVSC 531
QY 469 -----FVC-MCTISS-----CGIF----- 481
Db 532 WTCPCKENEYVDEYTCACQGLGSWPTDGLTGVYLIRWGDPEPIAAVVFACGLG 591
QY 482 --VAFALIFNWKHRRVIOSSHPVCNTIMLFGVII-----CLISVILLGIDGRFVSP 533
Db 592 LATLFVTVFIIYRDPVVKSSREL-C-YIILAGICLGLVCTFCLIA----- 637
QY 534 EEPKICQARAWLLSTGF---TLAYGAMFSKVMRVHRTTAKTDPRKKKVPKLYTMV 589
Db 638 --KPK--QIYCYLQRIQIGLSPAMSYSAVTKTNRIARLAGS-----KKKICTKKPRFMS 689
QY 590 SGLLSIDLVLISWQIFDPLQRYLETFFLEDPVSTDDIKIRPELEHESQSRNSMWGLV 649
Db 690 ACAQLVIAFLICIQ---LGIIVALFIMEPPDMDHYPISREVYLIC---NTNLGVV 741
QY 650 --YGFKGLILVFLGLFLAYETRSIKVKQINDSRVYVGMYSYNNVVLCLITAPVGMVIAQQD 707
Db 742 TPLGYNGLLILSCTFYAFKTRNPA-NFNEAKYIAFTMTTCIIWLAFVPI----- 791
QY 708 ASFAFVALAVIFCCF-----LSMLLIFVPKVIIVIRHPDKAKSKYNPDSAI----- 754
Db 792 --YFGSNYKIITMCFVSLSATVALGCMFVKYIILAKPERNVSATTTSTVVRMHVGD 849
QY 755 --SKDEERYOKLV-----TENEQ-----LQRL-----ITOKE 780
Db 850 GKSSSAASRSSSLNLMKRRGSSGETLRNGSKVSTWQAQNEKSSRGHLWQLSIHINKKE 909
QY 781 EKIRVLQRVLVERGDAKTENL-----CATGVASAAVATTSOPASLINS 825
Db 910 NP-----NQTAVIKFPFKSTESGLGPRGAGGAGGAGGAGGAGGPGP-----ES 960
QY 826 AHATPAATLAITQGE 840
Db 961 PDAGPKALYDAEAE 975

Db	817	WRH	--HYPTRDOVVLT-----	CNPDPHFLYSLAY--	DGFLVLVLTCTTYAVKTRK	861
Qy	670	IKVKQINDSRVYVMSIYVNVVCLITAPGVMTASQODSAFAFVALVAFCCFLSMILLIF	729			
Db	862	VP--ENFNETKFIQFSMYTTCVWLSWIFFFGTSGDFOIQTSSICISMSANVALACIF	920			
Qy	730	VPK--VIEVIRHP---KDKAESKNPDS-----	AISKEDERQKLVTEQQLQ	773		
Db	921	SPKLWILIFKHKVNRQEGESMLNKSRSIGNCSSRLCANSIDEPNOYTALLTIDSTR--	978			
Qy	774	RLITQKEEKIRVLQRRLVERGDKATGELNGATGVASAAVATTTSQASLINSSAHAT	829			
Db	979	-----RRSSRK-----	TSQPTFS--TSSAHT	997		

RESULT 15

A41939

G protein-coupled glutamate receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: A41939; S15362

R:Houramed, K.M.; Kuljper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J

Science 252, 1318-1321, 1991

A:Title: Cloning, expression, and gene structure of a G protein-coupled gl

A:Reference number: A41939; MUID:92022526

A:Accession: A41939

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-1199 <HOU>

A:Cross-references: GB:M61099; NID:g397806; PIDN:AAA19497.1; PID:g204460

A:Experimental source: cerebellum

A:Note: sequence extracted from NCBI backbone (NCBIP:60785)

R:Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.

Nature 349, 760-765, 1991

A:Title: Sequence and expression of a metabotropic glutamate receptor.

A:Reference number: S15362; MUID:91156047

A:Accession: S15362

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1199 <MAS>

A:Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1; PID:g56647

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	6.1%	Score 268;	DB 2;	Length 1199;
Best Local Similarity	18.8%;	Pred. No. 3.1e-12;		
Matches	168;	Conservative 146;	Mismatches 354;	Indels 228; Gaps
Qy	20	LIASPHLOGGVAGRPDELHIGGIPI	-----AKGGWGGQACMPATRLALD	66
Db	28	LLAGASSQSVARMGDGVIIIGALFVSHQPPAEKVPKPKGGEITREQYGIORVAMFHTLD	87	
Qy	67	DVNPQPNLLPGFKLILHSNDS--ECEPGLGASVMY---NLL-----	102	
Db	88	KINADPVLLPNTILGSEIRDSCHWSSVALEQSEIFRDSLISIRDEKGLNRCPLDPQQL	147	
Qy	103	----YNPQKMLMLAGSGTCTTVAEAKMWNLLVLCYGASSPALSRKRPFLFTRHPS	158	
Db	148	PPGRTRKPIAGVIGPGSSVAIQVNLLQLLFDIPQIAYSATSIDLSDKTYLYKFLRVVPS	207	
Qy	159	ATVHNPTRIKLWKFGSGRSVAILQAAEEVFISTVEDLENRCMEAGVEIVTRQSFSLSDPTD	218	
Db	208	DTLOARAMDILVKRYNTVYSAVTEGNYGESGMDAPKELAAQGLCIAHSDKIYSNAGE	267	
Qy	219	----AVNRLRQ--DARIIVGLEFVYVAARVLVCETKQOILYGRAHWFFFIQWYEDN---	268	
Db	268	KSFDRLLRKLRRUPKARVVVCFCEGTVTRGLLSAMRRILGVGVEFSLIGSDGWADRDEVI	327	
Qy	259	-WYEVNLIKAEGITCTVEQMRTAA-----EGHLTTEAL-----MNQNNQTTISGMTAE	315	
Db	328	EGYEVEANG-GITIKLASPEYRSFDDYFLKRLRLDTNTRNPFWPEFWQHRFQCRLLPGHLL	386	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:13:08 ; Search time 14.82 Seconds
(without alignments)
2078.168 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGAVTFWIFLLCL.....LINSSAHATPAATLAIQTGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2031.5	46.4	960	1	GBR1_MOUSE
2	2030.5	46.4	961	1	GBR1_HUMAN
3	2004	45.8	991	1	GBR1_RAT
4	1290	29.5	941	1	GBR2_HUMAN
5	1286	29.4	940	1	GBR2_RAT
6	366.5	8.4	976	1	MGR2_MOUSE
7	361	8.3	908	1	MGR2_RAT
8	360	8.2	908	1	MGR8_HUMAN
9	356.5	8.2	912	1	MGR4_RAT
10	355	8.1	908	1	MGR8_MOUSE
11	355	8.1	915	1	MGR7_HUMAN
12	353	8.1	912	1	MGR4_HUMAN
13	353	8.1	915	1	MGR7_RAT
14	334.5	7.6	871	1	MGR6_RAT
15	333	7.6	879	1	MGR3_RAT
16	323	7.4	877	1	MGR3_HUMAN
17	322	7.4	872	1	MGR2_HUMAN
18	318	7.3	872	1	MGR2_RAT
19	313.5	7.2	877	1	MGR6_HUMAN
20	305	7.0	1203	1	MGR5_RAT
21	297.5	6.8	1212	1	MGR5_HUMAN
22	294	6.7	999	1	MGR1_CAEL
23	276	6.3	1194	1	MGR1_HUMAN
24	268	6.1	1199	1	MGR1_RAT
25	227.5	5.2	1079	1	CASR_MOUSE
26	219.5	5.0	1078	1	CASR_HUMAN
27	212.5	4.9	1079	1	CASR_RAT
28	198.5	4.5	1085	1	CASR_BOVIN
29	184.5	4.2	1047	1	ANPB_RAT
30	181.5	4.1	1047	1	ANPB_BOVIN
31	177.5	4.1	1047	1	ANPB_HUMAN
32	172	3.9	1050	1	ANPB_ANGJA
33	159	3.6	540	1	ANPC_HUMAN

34	156	3.6	1061	1	ANPA_HUMAN	P16056	homo sapien
35	154	3.5	535	1	ANPC_RAT	P41740	rattus norv
36	147.5	3.4	1057	1	ANPA_RAT	P18910	rattus norv
37	146	3.3	1057	1	ANPA_MOUSE	P18293	mus musculus
38	145	3.3	1137	1	CYGL_CAEL	Q09435	caenorhabdi
39	144.5	3.3	536	1	ANPC_MOUSE	P70180	mus musculus
40	142	3.2	537	1	ANPC_BOVIN	P10730	bos taurus
41	137.5	3.1	836	1	GLK1_MOUSE	Q60934	mus musculus
42	137.5	3.1	1103	1	CYGF_BOVIN	Q02740	bos taurus
43	132.5	3.0	1108	1	CYGF_HUMAN	P51841	homo sapien
44	128	2.9	918	1	GLK1_HUMAN	P39086	homo sapien
45	128	2.9	1110	1	CYGX_RAT	P51839	rattus norv

ALIGNMENTS

RESULT	1
GBR1_MOUSE	
ID	GBR1_MOUSE STANDARD; PRT; 960 AA.
AC	Q9WV18; Q9WV15; Q9WV16; Q9WV17; Q9WU48;
DT	20-AUG-2001 (Rel. 40, Created)
DT	20-AUG-2001 (Rel. 40, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE	RECEPTOR 1) (GABA-B-R1) (GB1).
GN	GABBR1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RX	MEDLINE=20237752; PubMed=10773016;
RA	Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,
RA	Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA	Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT	"Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
RT	receptors with truncated receptors and metabotropic glutamate
RT	receptor 4 supports the GABA(B) heterodimer as the functional
RT	receptor.";
RT	J. Pharmacol. Exp. Ther. 293:460-467(2000).
RL	SEQUENCE FROM N.A. (ISOFORMS 1B; 1C AND 1D).
RN	[2]
RP	Younger R.;
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 1B).
RA	Lamp K., Humenay A., Nikolic Z., Becker C.-M.;
RT	"Cloning of the murine GABABR1b receptor.";
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RA	Humenay A., Lamp K., Nikolic Z., Becker C.-M.;
RT	"Mouse GABA-B receptor cDNA sequence.";
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	RIA-R2 INTERACTION.
RX	MEDLINE=99102694; PubMed=9872744;
RA	Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA	Kornau H.-C.;
RT	"Role of heteromer formation in GABAB receptor function.";
RL	Science 283:74-77(1999).
CC	-!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC	MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,
CC	STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC	INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC	INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC	FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC	GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC	HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC	GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC	INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE

HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND ANTINOCICEPTION. ACTIVATED BY (-)-BACLOFEN, CGP27492 AND BLOCKED BY PHACLOFEN.
 -!- FUNCTION: ISOFORM 1E FUNCTION MAY BE TO REGULATE THE AVAILABILITY OF FUNCTIONAL GABA-B-R1A/GABA-B-R2 HETERODIMERS BY COMPETING FOR GABA-B-R2 DIMERIZATION. THIS COULD EXPLAIN THE OBSERVATION THAT CERTAIN SMALL MOLECULE LIGANDS EXHIBIT DIFFERENTIAL AFFINITY FOR CENTRAL VERSUS PERIPHERAL SITES.
 -!- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO HAPPEN. ISOFORM 1E (WITHOUT C-TERMINAL INTRACELLULAR DOMAIN) IS UNABLE TO DIMERIZE VIA A COILED-COIL INTERACTION WITH GABA-B-R2. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE PLASMA MEMBRANE. ISOFORM 1E CAN ALSO BE SECRETED.
 -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A (SHOWN HERE), 1B, 1C, 1D AND 1E/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS CORRESPONDING TO THE FULL RECEPTOR ARE ESSENTIALLY FOUND IN THE CENTRAL NERVOUS SYSTEM (CNS). ISOFORM 1E IS THE MAJOR ISOFORM IN ALMOST ALL PERIPHERAL TISSUES. IT MAY ACT AS AN ANTAGONIST OF GABA-B RECEPTORS, BEING ABLE TO DISRUPT THE NORMAL ASSOCIATION BETWEEN ISOFORM 1A AND GABA-B-R2.
 -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND WEAKLY IN HEART, SMALL INTESTINE AND UTERUS. MOSTLY EXPRESSED IN GRANULAR CELL AND MOLECULAR LAYER FOR ISOFORM 1A AND IN PURKINJE CELLS FORM ISOFORM 1B. ISOFORM 1E IS PREDOMINANTLY EXPRESSED IN PERIPHERAL TISSUES AS KIDNEY, LUNG, TRACHEA, COLON, SMALL INTESTINE, STOMACH, BONE MARROW, THYMUS AND MAMMARY GLAND.
 -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE SPECIFICITY FOR G-PROTEIN COUPLING.
 -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. GABA-B RECEPTOR SUBFAMILY.
 -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

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 DR EMBL; AJ225028; CAA12359.1; -
 DR EMBL; AJ225029; CAA12360.1; -
 DR EMBL; AJ012185; CAA09939.1; -
 DR EMBL; AJ012186; CAA09940.1; -
 DR EMBL; AF099148; AAC98508.1; -
 DR EMBL; Y11044; -; NOT ANNOTATED_CDS.
 DR EMBL; AJ012187; CAA09941.1; -
 DR EMBL; AJ010170; CAA09031.1; JOINED.
 DR EMBL; AJ010171; CAA09031.1; JOINED.
 DR EMBL; AJ010172; CAA09031.1; JOINED.
 DR EMBL; AJ010173; CAA09031.1; JOINED.
 DR EMBL; AJ010174; CAA09031.1; JOINED.
 DR EMBL; AJ010175; CAA09031.1; JOINED.
 DR EMBL; AJ010176; CAA09031.1; JOINED.
 DR EMBL; AJ010177; CAA09031.1; JOINED.
 DR EMBL; AJ010178; CAA09031.1; JOINED.
 DR EMBL; AJ010179; CAA09031.1; JOINED.
 DR EMBL; AJ010180; CAA09031.1; JOINED.
 DR EMBL; AJ010181; CAA09031.1; JOINED.
 DR EMBL; AJ010182; CAA09031.1; JOINED.
 DR EMBL; AJ010183; CAA09031.1; JOINED.

DR EMBL; AJ010184; CAA09031.1; JOINED.
 DR EMBL; AJ010185; CAA09031.1; JOINED.
 DR EMBL; AJ010186; CAA09031.1; JOINED.
 DR EMBL; AJ010187; CAA09031.1; JOINED.
 DR EMBL; AJ010188; CAA09031.1; JOINED.
 Query Match 46.4%; Score 2030.5; DB 1; Length 961;
 Best Local Similarity 49.3%; Pred. No. 8.9e-148;
 Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
 QY 24 PHLQGGVAGRPDE--LHIGGIFPIAGGQGGQACMPATRLALDDVKNOPNLLPGFKLI 81
 Db 155 PHQOVNTPHSERRAVYIGALFPM--GGNPGGACQAPVEMAELEDVNSRDILDPYELK 212
 QY 82 LHSNDSECEPLGASVMNLYNKPQKMLLAGCSTVCTTVAEAAKMNLLVLCYGASSP 141
 Db 213 LIHDSKCDPGQATKYLYELLYNDPIKIILMPGSSVSTLVAEAAKMNLLVLSYGSSP 272
 QY 142 ALSDRKFPFLFRTHPSATVHNPTRIKMKFGHSRVAILQOAEVEFISTVEDLENCRME 201
 Db 273 ALSNRQRPFTFFTHPSATLHNPTRVKLFKMGWKKIATIQOITTEVFTSLDDLEERVKE 332
 QY 202 AGVEIVTRQSFSLDPTDAVNLNRDARIIVGLFVVAARVLCMYKQOOLYGRAHWFF 261
 Db 333 AGIEITFRQFFSDPAVPVNLKQDARIIVGLFYEARKVCEYKLERLFGKYYWFL 392
 QY 262 IGWYEDNMYEVNLKAEGITCTVEOMRIAAEGHLETEALMNNQNTTISGMTAEFEHRRL 321
 Db 393 IGWYADNWFKI--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRTSNNTSQEFVEKL 450
 QY 322 NQALIEGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKMTMERLITGKKSIRDYIT 378
 Db 451 TKRL-----KRHPETGGFQEAFLAYDAIWAALALNLTSGGGSGRVRLEENYN 501
 QY 379 DKEIADIEYAAAMSTQFLGVSGVVAFFSQGDRIALTOEQMIDCKEYKLYDYDQDNLS 438
 Db 502 NQITDQIYRAMNSSSEFVGHVVDASGRMAWTLEQLQGGSYKKYGYDSTKDDL 561
 QY 439 WLNTQEWIGGKVPQDRTIVTHLVTSPLFVCMCTISSCGIFVAFALIIFNWNKHRRV 498
 Db 562 WSKTDKWWGGPPADQTLVTKTRFLSOKLFISSVLSLSGLVLAIVCLSFNINSHVRY 621
 QY 499 IQSHPCVNTIMLFGVILICLISVILLGIDGRFVSPPEVPKICQARALLSTGFTLAYCAM 558
 Db 622 IQNSQPNLNLTAVGCSLAAVFLGLDGYHIGNQFPFVFCQARLMLLGLGFSILGSGM 681
 QY 559 FSKVMRYHREFTTK--AKTDPKKKVPWKLYTMVSGLLSIDLVLLSQIFDPLQRYLET 616
 Db 682 FTKIWWVHTVFTKKEKKEKWKLTLEPKLYATVGLLVGMDVLTALWQIVDPLHRTIETF 741
 QY 617 PLEDVSTTDDIKIRPELEHCEQSNMGLVYGFKGLILVFLGFLAYETRSIKVQIN 676
 Db 742 AKEPKREDI-DVSILPQLEHCSSRKMTWLGFYGYKGLLLGLLGLLAYETKSVSTEKIN 800
 QY 677 DSRVVGMSIYVNVVLCITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFFPKVIEV 736
 Db 801 DHRAVGMAIYNVAVLCITAPVTMILSSQDQAAFAFASLAIVFSYITLVLFVFKMRL 860
 QY 737 IRHP--KDKAESKYNPDSAIKDEERYQKLVTEQOLRLITQKEKIRVLRORLVER 793
 Db 861 ITRGEWQSAQDTMKTGSSSTNNNEEKSRLLEKENRELEKIAEKEKRVSELHOLQSR 919
 RESULT 3
 GBRL_RAT
 ID GBRL_RAT STANDARD; PRT; 991 AA.
 AC Q9Z004; O08620; O08621; Q9Z0F9; Q9Z308;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B RECEPTOR 1) (GABA-B-R1) (GB1).
 GN GABBR1.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC STRAIN-RICO; TISSUE-Brain cortex, and Cerebellum;
 RX MEDLINE=97222131; PubMed=9069281;
 RA Kaupmann K., Hugdel K., Heid J., Flor P.J., Bischoff S., Mickel S.J.,
 RA McMaster G., Angst C., Bittiger H., Froestl W., Bettler B.;
 RT "Expression cloning of GABA(B) receptors uncovers similarity to
 RT metabotropic glutamate receptors.";
 RL Nature 386:239-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).
 RC TISSUE-Cerebellum;
 RX MEDLINE=99092370; PubMed=9875211;
 RA Isomoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,
 RA Yano K., Taniyama K.;
 RT "Cloning and tissue distribution of novel splice variants of the rat
 RT GABAB receptor.";
 RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1E).
 RC STRAIN-Wistar; TISSUE-Hippocampus;
 RX MEDLINE=99388283; PubMed=10457184;
 RA Pfaff T., Malitschek B., Kaufmann K., Prezeau L., Pin J.-P.,
 RA Bettler B., Karschin A.;
 RT "Alternative splicing generates a novel isoform of the rat
 RT metabotropic GABA(B)R1 receptor.";
 RL Eur. J. Neurosci. 11:2874-2882(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1A), AND R1A-R2 INTERACTION.
 RC TISSUE-Brain;
 RX MEDLINE=99175124; PubMed=10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity.";
 RL J. Biol. Chem. 274:7607-7610(1999).
 RN [5]
 RP TISSUE DISTRIBUTION.
 RX MEDLINE=20121644; PubMed=10658574;
 RA Balley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,
 RA Ng G.Y.K.;
 RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP
 RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor
 RT forms.";
 RL Bioorg. Med. Chem. 7:2697-2704(1999).
 RN [6]
 RP R1A-R2 INTERACTION.
 RX MEDLINE=99102694; PubMed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of Heteromer Formation in GABA-B Receptor Function.";
 RL Science 283:74-77(1999).
 RN [7]
 RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.
 RX MEDLINE=20159055; PubMed=10692480;
 RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,
 RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,
 RA Kaupmann K., Pin J.-P.;
 RT "Binding at GABA(B) receptors: involvement of serine 269 of the
 RT GABA(B)R1 subunit.";
 RL Mol. Pharmacol. 57:419-426(2000).
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE

CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION.
 CC -1- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A, 1B, 1C, 1D AND 1E (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN
 CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL
 CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS, GRANULAR CELL
 CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM
 CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).
 CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS
 CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY
 CC BLADDER.
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC -1- CAUTION: ISOFORM 1E HAS BEEN CALLED 1C IN REF. 3.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC -----
 CC EMBL; Y10369; CAA71398.1; -;
 CC EMBL; Y10370; CAA71399.1; -;
 CC EMBL; AB016160; BAA34708.1; -;
 CC EMBL; AB016161; BAA34709.1; -;
 CC EMBL; AF110797; AAD19656.1; -;
 CC EMBL; AF110796; AAD19655.1; JOINED.
 CC EMBL; AF110797; AAD19657.1; -;
 CC EMBL; AF110796; AAD19658.1; JOINED.
 CC EMBL; AF110796; AAD19658.1; JOINED.
 CC EMBL; AF110797; AAD19659.1; -;
 CC EMBL; AF110796; AAD19659.1; JOINED.
 CC HSSP; P10998; IVVC.
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00003; 7tm_3; 1.
 CC Pfam; PF01094; ANF_receptor; 1.
 CC Pfam; PF00084; sushi; 2.
 CC PRINTS; PR01176; GABABRECEPTR.
 CC PRINTS; PR01177; GABABRECEPTR.
 CC SMART; SM00032; CCP; 2.
 CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.
 KW

FT	SIGNAL	1	16	POTENTIAL.	
FT	CHAIN	17	991	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1.	
FT	DOMAIN	17	590	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	591	611	I (POTENTIAL).	
FT	DOMAIN	612	630	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	631	651	II (POTENTIAL).	
FT	DOMAIN	652	666	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	667	687	III (POTENTIAL).	
FT	DOMAIN	688	709	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	710	730	IV (POTENTIAL).	
FT	DOMAIN	731	797	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	798	818	V (POTENTIAL).	
FT	DOMAIN	819	834	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	835	855	VI (POTENTIAL).	
FT	DOMAIN	856	863	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	864	884	VII (POTENTIAL).	
FT	REPEAT	29	95	SUSHI 1.	
FT	REPEAT	99	156	SUSHI 2.	
FT	DOMAIN	885	991	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	901	955	COILED COIL (POTENTIAL).	
FT	CARBOHYD	23	23	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	408	408	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	481	481	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	513	513	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	VARSPLIC	1	163	MULLILPLPLPLAGAGGAOTNATSEGOIHPWEGGIR YGLTRDVKATNPLVDYIEVCRGEEVGVKPKYKCLANSGWTDMDTPSCVRCIKSYLTLENGKVELFGDPLDAG ARVEFCDPDLVLGSSRSVQOGWSTPKPHQVNRTPH -> MGPGPCTVGNPLPLLLVMAAGVAPVWASHSLPRP HPRVPHPHS (IN ISOFORM 1B, ISOFORM 1C AND ISOFORM 1D).	
FT	VARSPLIC	771	801	MISSING (IN ISOFORM 1A, ISOFORM 1B AND ISOFORM 1D).	
FT	VARSPLIC	935	991	KEERVELRHQLQSRQLRRHPPTPPDPSGGLPRGPSEP PDLSCDSGRVHLLYK -> VCGDKQGPVPSGGLPVVGP STEV (IN ISOFORM 1D).	
FT	MUTAGEN	247	247	S->A: NO CHANGE IN THE AFFINITY FOR GABA.	
FT	MUTAGEN	268	268	S->A: NO CHANGE IN THE AFFINITY FOR GABA.	
FT	MUTAGEN	269	269	S->A: DECREASE IN THE AFFINITY FOR GABA.	
SQ	SEQUENCE	991 AA;	111533 MW;	012CD293D4B44A2 CRC64;	
Query Match					45.8%; Score 2004; DB 1; Length 991;
Best Local Similarity					47.5%; Pred. No. 1e-145;
Matches 385; Conservative 152; Mismatches 219; Indels 54; Gaps 9;					
QY	24	PHLQGVAGRPDE--LHIGIFPIAGKGWGGQACMPATRLALDDVKNQPNLLPGFKLI	81		
DB	154	PHQVNRTPSHERRAVYIGALFPMS--GGWPGGQACQAPVEMALEDVNSRRDILPDVELK	211		
QY	82	LHSNDECEPGLGASVWYNNLYNKPDKMLLACGCTVCTTVAEAKMWNILVLCYGASSP	141		
DB	212	LJHDSKCDPGQATKYLYELLYNDPKIKIILMPGSCSVSTLVAEAAAMNVLVLSYGSSP	271		
QY	142	ALSDRKREFTLPRTPTSATVHNPTRIKLMKFCWSRAIILQQAEEVFISTVEDLENRCME	201		
DB	272	ALSNRORFTFFTHPSATLHNPTRIKLFKWKGNKIATIQQTEVFSTLDDLEERKE	331		
QY	202	AGVEIVTROSFSLSDPTDAVRNLRRDARIIVGLFYVVAARRVLCEMYKOOLYGRAHWYFF	261		
DB	332	AGIEITFRSFFSDPAVPVKNLKRQDARIIVGLFYETEARKVCEVYKERLFGKKYWFEL	391		
QY	262	IGWYEDNWEVNLKAGSITCTVQOMRIAEGHITLREALMWNQNNQTTISGMTAEFEHRFL	321		
DB	392	IGWYADNWEFT--YDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSISNNTSQEFVEKL	449		
QY	322	NQALIEEGYDINHRYPE---GQOEAPLAYDAVWSVALAENKMTWERTTCKKSLRDTYTT	378		
DB	450	TKRL-----KRHPETGGFQOEAPLAYDAIWALALANKTSGGGGSGVRLEDNFYN	500		

QY	379	DKEIADRIYAMNSTOFLGYSVGVAFSSQGDRIALTQIEQMIDKYEKLGYYDTOLDNLS	438		
DB	501	NOTITDQIYRAMNSSSEFVGHVYFDASGRMAWTIEQLQGGSYKKIGYDSTKDDLS	560		
QY	439	WLNEQWIGGKVPQDRIVTHVTRVSLPLFCVCMCTSSCGIFVAFALIIENIWNKHRRV	498		
DB	561	WSTDKWIGGSPADQTLVTKTFRFLSQKLFISVSVLSSGLIVLAVCLSNINSHVRY	620		
QY	499	IQSSHPVCNTIMLFGVIICLISVILLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYGAM	558		
DB	621	IQNSQPNLNLTAVGCSLAAAVPLGLDGVHIGRSQFPFVCQARLWLLGLGSLGYSGM	680		
QY	559	FSKVRVHRFTTK--AKTDPKKKVPKLYTWMSGLSIDLVILLSWQIFDPLQRYLETFF	616		
DB	681	FTKIWWVHTVFTKKEKKWKRTLEPKLYATVGLLVGMVLTLLAIWQIVDPLHRTIETF	740		
QY	617	PLEDPVSTTDDIKIRPELHCECSORNSMWLG-----	647		
DB	741	AKEPKEDI-DVSLPQLCHCCKRMNTWLGELMSFAVSSDVQRATVGGDSPICVWPAP	799		
QY	648	--LVYFGKGLILVFLGLAYETRSIKVKQINDSRYVGSIIYNNVVVLCILITAPVGMVIASQ	705		
DB	800	ESIFYGKGLLLGIFLAYETKSVSTEKINDHRAVGMALYVNAVCLITAPVTMILSSQ	859		
QY	706	QDASFVAVLAVIFCCFLSMLLIIVPKVIEVIRHPKKAESK--YNPDSALSKDEERYQ	763		
DB	860	QDAFAFASLAIVSSYITLVVLEVPKMRRLITRGWQSETQDTMTKSTGNNNEEKS	919		
QY	764	KLVTENQLOQLRNLQKEEKIRVLRORLVER	793		
DB	920	LLEKENELEKIIAEKEKRVSELRHQLQSR	949		
RESULT 4					
GBR2_HUMAN STANDARD; PRT; 941 AA.					
ID	GBR2_HUMAN	STANDARD; PRT; 941 AA.			
AC	O75899; O75974; O75975; O9UN99; O9UNR1; Q9P1R2;				
DT	20-AUG-2001 (Rel. 40, Created)				
DT	20-AUG-2001 (Rel. 40, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR 51) (GPR 51) (HG20).				
GN	GABBR2 OR GPR51.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 2A).				
RC	TISSUE=Cerebellum;				
RX	MEDLINE=99087321; PubMed=9872316;				
RA	White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,				
RA	Barnes A.A., Emson P., Foord S.M., Marshall F.H.;				
RT	"Heterodimerization is required for the formation of a functional				
RT	GABA(B) receptor.";				
RL	Nature 396:679-682(1998).				
RN	[2]				
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).				
RC	TISSUE=Brain;				
RX	MEDLINE=20193514; PubMed=10727622;				
RA	Clark J.A., Mezey E., Lam A.S., Bonner T.I.;				
RT	"Distribution of the GABA(B) receptor subunit gb2 in rat CNS.;"				
RL	Brain Res. 860:41-52(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 2A).				
RA	Liu M., Parker R., McCrear K., Watson J., Baker E., Sutherland G.,				
RA	Herzog H.;				
RT	"Cloning and characterization of a novel human GABA-B receptor subtype				
RT	with high affinity for GABA and low affinity for baclofen.";				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				

Query Match 29.5%; Score 1290; DB 1; Length 941;
Best Local Similarity 33.9%; Pred. No. 6.2e-91;
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;

Qy 18 LCLIASPHLQGVAGRP-----DELHIGGIPPI---AGKGGWGGGOACMPATRLALDDV 68
Db 31 LLLPLAPGAWGARGAPPPSPPLSINGLPLKEVAKGSI--GRGVLPVELAIEQI 88
Qy 69 NKQPNLLPFGKLLHNSDECEPGLGASVYNNLLNPKQKMLLAG-CSTVCTTVAEAAK 127
Db 89 RNESLLRPVF-LDLRLYTECONANGKAFYDAIKYGNHLMVFGVCPSPVTSIIAESLQ 147
Qy 128 MWNLVICYGASSPALSRRPPTLFTPTSPATVHNPTRIKLMKKKGSWRAVILQAAEV 187
Db 148 GWNVLQSFSAATTPVLAADKKYFYFRTVPSDNVNAVPAIKLLKHQWKRVGTLQDVQR 207
Qy 188 FISTVEDLENRCMEAGVEITVTRQSFSLSDPTDAVRLRRDARLIIVGLFYVVAARRVLC 247
Db 208 FSEVRNDLTGVYGEDIELSDTESFSDPCTSVKKLGKNDVRIILGQFQDNMAAKVPCA 267
Qy 248 YKQQLYGRAHVWFFVYEDNNYE-VNLKAEGITTCVEQWRTAAEGHLTEALMWNQNNQ 306
Db 268 YEENYGSYQWIFPCWEPSEWQVHTTEANSRCLRNLLAAEGYIGVDFEPLSKQI 327
Qy 307 TTISGMTAEFRHLRNQALIEGYDINHDPYEGYQEAFLAYDAVMSVALAFNKTMERL- 365
Db 328 TTISGMTAEFRHLRNQALIEGYDINHDPYEGYQEAFLAYDAVMSVALAFNKTMERL- 365
Qy 328 TTISGMTAEFRHLRNQALIEGYDINHDPYEGYQEAFLAYDAVMSVALAFNKTMERL- 365
Db 328 TTISGMTAEFRHLRNQALIEGYDINHDPYEGYQEAFLAYDAVMSVALAFNKTMERL- 365
Qy 366 -TTGKSLRDFTYTDKEIADEIYAAMNSTOFLGVSGVAFSSQDRIALTOIEQMDGKY 424
Db 378 ASSRHQIQDFNYDHTLGRILNANMETNFFGVTVGVVFRN-GERMTIKFTQFQDSRE 436
Qy 425 EKLGYDITOLDNLMLN-TEOWIGGKVPQDRTIVTHVLRVSLPLFCMCTISSCGLEFA 483
Db 437 VKVGEYNAVADTLEINDTIRFGSEPPKDKTILQLRKLISPLSILSALTILGIMA 496
Qy 484 FALIIFNWKHRRVITQSHHPVCNTIMLFGVILCLISVILGIDGRFVSPPEEPKICQAR 543
Db 497 SAFLEFNKRNQKLIKMSYPMNNLILGGLMSYASIFLGLDGSFVSEKTFETLCTVR 556
Qy 544 AMLLSTGFTLAYGAFSKVWRVHRTTKAKTPKKVPEWPKLYTMVSGLLSIDLVILLWS 603
Db 557 TWILVGYTAFGAFKPTWRHAFKVKM-KKKTIKDKQLLVIVGGMLLIDLCILICW 615
Qy 604 QIFDPLQRYLETFFLE-DEPVSTDDIKIRPELEHCEFSORNSMGLVYGFGLILVGLF 662
Db 616 QAVDPLRTRVEKYSMEPDAGR--DISIRPLEHCENTHTWILGIVYAYKGLMLFGCP 673
Qy 663 LAYETRSIKVKQINDSRVYGMISYNNVVLCTAPYGVMIASQODASFAFVALAVIFCCF 722
Db 674 LAWETRNVSIPALNDSKYIGMSYNNVINGIICAAVSFLTRDQPNQVFCIVALVIFCST 733
Qy 723 LSMILFVPKVIETVIRHP-----KDKAESKNPD-SAIKSEDEERYQKLV 767
Db 734 ITLVLFVPEKLTIRNPDAATQNRFRFQTONOKEDSKTSTSVTSYNQASTSRLEGLOS 793
Qy 768 ENEOQLRLTOKEEKIRVLRVERGDAKT-----ELNGATCVASAAVATTSSOPA 819
Db 794 ENHRLUMKTELKDLLEVTMLQDTPPE-KTYYIKONHVOELNINLGNFTSTEDGGKA 852
Qy 820 SLIN 823
Db 853 ILKN 856

RESULT 5
ID GBR2_RAT STANDARD; PRT; 940 AA.
AC O88871: Q9QWU2: Q9JK36;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).
GN GABBR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus; PubMed=9872315;
RX MEDLINE=99087320; PubMed=9872317;
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,
RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
RA Salton J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,
RA Branchek T.A., Gerald C.;
RT "GABA(B) receptors function as a heteromeric assembly of the subunits
RT GABA(B)R1 and GABA(B)R2.";
RL Nature 396:674-679(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex, and Cerebellum;
RX MEDLINE=99087320; PubMed=9872317;
RA Kaupmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P.,
RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
RA Bettler B.;
RT "GABA-B receptor subtypes assemble into functional heteromeric
RT complexes.";
RL Nature 396:683-687(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP R1A-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.
RC TISSUE=Hippocampus;
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of Heteromer Formation in GABA-B Receptor Function.";
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CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPARTED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCICEPTION.
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
CC HABENULA, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
CC CEREBELLUM.

RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=96421661; PubMed=8824309;
RA Parentier M.L., Pin J.P., Bockaert J., Grau Y.;
RT "Cloning and functional expression of a Drosophila metabotropic
RT glutamate receptor expressed in the embryonic CNS.";
RL J. Neurosci. 16:6687-6694(1996).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CNS OF THE LATE EMBRYO.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X99675; CAA67993.1; .
DR GCRDb; GCR_1123; .
DR FlyBase; FBgn0019985; Glu-RA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMRG.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
DR PROSITE; PS00983; G_PROTEIN_RECEP_F3_5; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 976 METABOTROPIC GLUTAMATE RECEPTOR.
FT DOMAIN 26 626 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 627 649 I (POTENTIAL).
FT DOMAIN 650 663 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 664 684 II (POTENTIAL).
FT DOMAIN 685 695 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 696 714 III (POTENTIAL).
FT DOMAIN 715 728 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 729 739 IV (POTENTIAL).
FT DOMAIN 760 782 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 783 804 V (POTENTIAL).
FT DOMAIN 805 817 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 818 840 VI (POTENTIAL).
FT DOMAIN 841 850 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 851 876 VII (POTENTIAL).
FT DOMAIN 877 976 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 229 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 524 524 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 976 AA; 108457 MW; 2C17B1F9005AF6F8 CRC64;

Query Match 8.4%; Score 366.5; DB 1; Length 976;
Best Local Similarity 19.7%; Pred. No. 5.3e-20;
Matches 203; Conservative 164; Mismatches 383; Indels 281; Gaps 40;

QY 3 KDMTSDGATWIFLCL-----IASP-----HLQGGVA-GRPDELHIGGIPPIAGKGNQ 53
DB 2 KQNNNGTILVVMVLSWSRVDLKSPTNTHQDSVSLPGDIIILGLFPVHEKG---E 58
QY 54 GQACMP-----ATRLALDDYNKOPNLLPGFKLILHSNDS----- 87
DB 59 GAPCGPKVYNRGVRLEAMLYAIDRVNDPNILPGITIGVHILDTCSDRYALNQLQV 118

QY 88 -----ECEPGIGASVMYNNLLYNKPKQLMLLAGCSTVCTTVAEAAKMNLIIVLC 135
DB 119 RASLNNDTSGYECADGSSPOLRKN-ASSGPFVFGVIGSSVSLQVLANLRLEPHPOVS 177
QY 136 YGASSPALSQRKRPPTLFRTHPSATVHNPTRIKLMKFGWSRVAILQAOAEVFISTVDL 195
DB 178 PASTAKTSLDKTRDFLARTVPPTFQSFVALVDILKNFNWSYVSTIHSSEGYGEVGEAL 237
QY 196 ENROMEAGVEIVTRQSFLSDPTDAV-----RNLRRODARIIVGLVYVVAARRVCEMYK 249
DB 238 HKEATERNVCIATAEKVPSAADDKVFDSIIISKLQKPNARGVLFTRAEDARRIL----- 292
QY 250 QQLYGRAHVFFIGWY-EDNWEYVNLKAEGL-----TCTVE-QMRTAAE-----GHLT 296
DB 293 -QAAKRLANLTOPFHWIASDGMGKOOKLEGLIEDIAEGAITVELQSEIADFRYMMOLT 351
QY 297 E-----ALMW-----NONNOTTISGMTAEERHRLNOALI 326
DB 352 ETNORNPFAYEWEDTFCNVLTSLSVKPDTSNSANSTDNKIGVKAKTECDSDYRLSEKV- 410
QY 327 EEGYDINHRYPEGYQEAFLAY--DAVMSVALAF-----NKTMERLTGKSLRDF 376
DB 411 --GYE-----QESKTOFVVDVAVAFAYALHNLHNDRCNTQSDQTTETRKHLSQES 458
QY 377 YDKEIADEIYAA-----MNSTQFLCVSG-VVAFSSQGRDIALTOI-- 416
DB 459 VVYRKISTDTKSQACPDMAVYDGEFNYNLLANVSFIDLAGEYKFDQGGDLARYDILN 518
QY 417 ----EQMIDGKYEKLYGYDTOLDNLSWLNTEBOWIGGKVPQDRTIVTHVLRVSLPLFCM 472
DB 519 YQOENSSGYQYKVIKWFENGLQ-----LNSETVVNNKETEPT-----SACSLPCEVGM 568
QY 473 -----C-----TISCG-----IF 481
DB 569 IKKQGGDTCWCWICDSCSEFEVYDEFTCKDCGPGLPYADKLSVALDIQYMKWNSLFL 628
QY 482 VAFALIIPNI-----WNKHRRYIQSSHVPVNTIMLFGVILICLISVILLIGDRF 530
DB 629 IPMAIAIFGIALTSIVIVLEFAKNHDTPLVRASGRELSYTLILFGILVCYCNFTAL- 682
QY 531 VSPEYPKI--COARWLISGFTLAYGAMFSKVRVHR-FTTKAKTDPK-KKVEPWKLY 586
DB 683 ---IAKPTIGSCVLRFGIGVGFSIIYSALLTKNRIHFHSKASKAQRUKYISPSQV 739
QY 587 TWSGLSLIDLVLISWQIFDPLQRYLETFFLEDPVSTDDIKIRPELEHCEQSQRNSMWL 646
DB 740 VITTSIAIQVILITMIMWVVEP-----PGTFYYPDRREVILCKIQDMSFLF 787
QY 647 GLVYGFGLILVFLGLFLAYETRSKVKQINDSRVGMYSIYVNVLCITAPVGMVIAQQ 706
DB 788 SOLYNN--ILITICTIYAIAKTRKIP-ENFNESKPIGFTMTYTCTIWLAFAPYFETGNSY 844
QY 707 DASPAFVALAIFCCFLSMILLIFVPKVIEWIRHPKDAESKYNPDLSAISKEDEERYOKLV 766
DB 845 EVQTTTICISLSASVALVCLYSPKVIILVFP-CKNVRKLTWNSTVYRKSAAVAAGA 903
QY 767 TENPQLORLIQKEEKIRVLRQLVERGDAGKTE-LNG---ATGVASAAVATTSP----- 818
DB 904 PTSSGYSRT-----HAPGTSALTGAVGTNASSSTLTQNSPHLDE 944
QY 819 ASLINSNAHAT 829
DB 945 ASAQTNVAHKT 955
RESULT 7
MGR8_RAT
ID MGR8_RAT STANDARD; PRT; 908 AA.
AC P70579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.

ID MGR8_HUMAN STANDARD; PRT; 908 AA.
 AC O00222; Q15493; O95945; O95946;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
 GN MGR8 OR GPRC1H OR MGLUR8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=98141892; PubMed=9473604;
 RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
 RA Rostack P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
 RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
 RT molecular cloning, functional expression, and comparison of
 RT pharmacological properties in RGT cells";
 RL Brain Res. Mol. Brain Res. 53:88-97(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=97446143; PubMed=9299241;
 RA Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.-C.;
 RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
 RT disproportionately large gene located at 7q31.3-q32.1.";
 RL Genomics 44:232-236(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
 RX TISSUE=Fetal brain;
 RA Malherbe P., Kratzelisen C., Lundstrom K., Richards J.G., Faull R.L.M.,
 RA Muter V.;
 RT "Cloning and functional expression of alternative spliced variants of
 RT the human metabotropic glutamate receptor 8";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDAJ databases.
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U92459; AAB51764.1; -;
 DR EMBL; U95025; AAB72040.1; -;
 DR EMBL; AJ236921; CAB36968.1; -;
 DR EMBL; AJ236922; CAB36969.1; -;
 DR GCRDb; GCR_1889; -;
 DR GCRDb; GCR_2604; -;
 DR MIM; 601116; -;
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PRINTS; PR01058; MTABOTROPICR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Olfaction; Alternative splicing.
 FT SIGNAL 1 33
 FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.

FT	DOMAIN	34	583		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	608		I (POTENTIAL).
FT	DOMAIN	609	620		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	621	641		II (POTENTIAL).
FT	DOMAIN	642	647		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	648	668		III (POTENTIAL).
FT	DOMAIN	669	695		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	696	716		IV (POTENTIAL).
FT	DOMAIN	717	746		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	747	768		V (POTENTIAL).
FT	DOMAIN	769	781		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	782	803		VI (POTENTIAL).
FT	DOMAIN	804	818		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	819	843		VII (POTENTIAL).
FT	DOMAIN	844	908		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	95	95		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	298	298		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	452	452		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	480	480		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	565	565		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	893	908		TSSTKTYISYNSHSI -> SKSVPEPPMYKSGSTS (IN ISOFORM B).
FT	VARSPLIC	454	501		SAGTPVTENENGDAAGRYDIFQYQITNKSTYKVGHWTNQ
FT					LHLKVED -> CARGIQMSLPWTLFTPSFSSSWAVALLLS
FT					LMKTEMLLDVMISSSIK (IN ISOFORM C).
FT	VARSPLIC	502	908		MISSING (IN ISOFORM C).
FT	CONFLICT	194	194		R -> A (IN REF. 2).
FT	CONFLICT	460	460		T -> I (IN REF. 2).
FT	CONFLICT	642	642		A -> G (IN REF. 2).
FT	CONFLICT	768	768		I -> N (IN REF. 1).
FT	CONFLICT	904	904		S -> T (IN REF. 2).
SQ	SEQUENCE	908 AA;	101740 MW;	95CD5883DAFGFDE	CRC64;

Query Match 8.2%; Score 360; DB 1; Length 908;
 Best Local Similarity 21.1%; Pred. No. 1.5e-19;
 Matches 204; Conservative 153; Mismatches 378; Indels 232; Gaps 44;

QY	13	FWIFLLCIAASPHLQGGVAG-RPD-ELHIGGIFPIAGKGGWQQGQAC-----MP	59
DB	22	YWI--LTMQRTSQEYAHRSIRVDGDIILGLFPVHAKG--ERGVPCGELKKEGIHRL	77
QY	60	ATRLALDDVKNQPNLLPGFKL---IL-----HNSDSECEPL	93
DB	78	AMLYAIDQINKDPDLSNITLGVRIIDTCSRDYVLEQSLTFVQALIEKADSVKANGD	137
QY	94	GASVYNLLNKKPKL--MLLAGCSTVCTTVAEAKMNLIVLCYGASSPALSDDKRPPT	151
DB	138	PP-----IFTKPKISGVIGAAASSVIMVANILRLFKIPQISYASTAPELSDNTRYDF	191
QY	152	LFRTHPSATVHNPTRIKLMKFGMSRVAILQQAEEVFSTVEDLENRCME-AGVEIVTRQ	210
DB	192	FSRVVPPDSQAQAMVDIVTALGNVYVSTLASEGNYGESGVEAFTQISREIGGVCIASQ	251
QY	211	SFLSDPTDA-----VRNLRQDARIIVGLFYVVAARRVLCEMYKQOLYGRAHWWFFIG	264
DB	252	KIPREPRGEFEKTIKRLLTTPNARAVIMFANEDIRILEAKKLNQSGH---FLWIG-	307
QY	265	YEDNW-----YEVNKAEGITCTVEQMRTAAG---HLTTEALMNQNNQTTISGMTA	314
DB	308	-SDSWGSKIAPVYQOEETIAG-AVTILPKRASIDGDFRYFRSRTLANNRRV-----	360
QY	315	EEFRHRLNQAIEEGYDINHRYPEGY-----OEAPLAY--DAVWSVALAFNKT	362
DB	361	EFWEENFGCKLGGSHGKRNHIKCTGLERTARDSYBOEGKVQFVIDAVYSMAVALHNMH	420
QY	363	ERLTGKKSL--RDTVTYDKIEADIEAAMNSTQFLGVSGV-VAFSSOGDIALTOIRQ-	418
DB	421	KDLCPGVIGLCPRMSTIDGKELLYIRA---VNFNSAGTPTVFENENGDAAGRYDIFQY	476
QY	419	MIDGK----YEKLGYYDTQL-----DNLSWLNTEQWIGGKVPQDRTIVTHVLTSLP----	467
DB	477	QITNKSTYKVGHWTNQHLKVEDMQWAHREH-----THPASCVSLPCKPG	523

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QY 468 -----LFVCMCTI-----SSC----- 478
DQ 524 ERKKTGVPCWCERCEGYNOYDELSCELCPLDQRPNNMRTGCQLPIIKLEWHSWP 583
QY 479 --GIEVA-----FALIIFNTWKKHRRVIOSSHPCVNTIMLFGVILCLISVILLGTD 527
DQ 584 AVPVFVAILGIIATTFVIVTFVRYN-DTPIVRASGRELSYVLLTGIFLCYSITFILM--- 639
QY 528 GRFVSPEYPRKICARALLSTGETLAYGAMFSKVMRVRHRTTAK---TDPKKKVPEWK 584
DQ 640 --IAAPDTI--ICSFRRVFLGCMCFSAALLTKNRHRIFFEQCKSVTAP-KFISPAS 694
QY 585 LYTMVSGLLSDLVLLISQWIFDPLORYLFTPELDPVSTTDDIKIRPELEHCEQSQRNSM 644
DQ 695 QLVTFSLISVOLLGVFWFVVDPPHIID---YGEQRTLDPEKARGVLK-CDISDLSL 749
QY 645 WLGLVYGEKGLIIVGLFLAYETRSIKVKQINDSRVGMYSYVNVVGLLITAPVGMVIAS 704
DQ 750 ICSSL--GYSILLMTCTVYAIKTRGVP-ETFNKAPIGFTMYTTCIILAFIPFPGTAQ 806
QY 705 QODASE--AFVALAVIFCCFLSMILIFVPKVIEWIRHPKDKAESKYNPDSAISKEDEER 761
DQ 807 SAEKMYIQTTLTVMSLSASVSGLMLYMPKVYIIFHPQONVQKR-----RKS 855
QY 762 YQKLVTENEQLRLITKEERIRVLQRQLVERGDAKGTGLNGATGVASAAVATTSPASL 821
DQ 856 FKAVVTAATMSKLIQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTY 900
QY 822 INSSAHA 828
DQ 901 ISYNSHS 907

RESULT 9
MGR4_RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M92077; -; NOT_ANNOTATED_CDS.
CC EMBL; M90518; AAA93190.1; -.
CC PIR; JH0563; JH0563.
CC GCRDb; GCR_0352; -.
CC GCRDb; GCR_0363; -.
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRGR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01054; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
CC PROSITE; PS00983; G_PROTEIN_RECEP_F3_5; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 610 I (POTENTIAL).
FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 124 124 Q -> R (IN REF. 2).
SQ SEQUENCE 912 AA; 101818 MW; 336430EF19B4B577 CRC64;
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Query Match 8.2%; Score 356.5; DB 1; Length 912;
Best Local Similarity 18.9%; Pred. No. 2.8e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

QY 5 MTSDCGAVTEW--IFLLCLIAS-----PHLOGGAGRP-----DELHIGGFIACK 48
DQ 1 MSGKGGWAWMARLPICLLLSIYAPWVPSLSGKPKGPHMNSIRIDGDTLGGFLFVHGR 60
QY 49 GCWQGGQAC-----MPATRLALDVKNPQMLPGFKL----- 80
DQ 61 G--SEGKACGELKKEGIIHRLAMLFALDRINNDPDLNITILGARILDTCSRDTHALEQ 118
QY 81 -----ILHNSDSECEPGLGASVMYLNLYNKPQKMLLAGC--STVCTTVAEAKMWNL 131
DQ 119 SLTFVQALIEKDGTEVRCGGGPP-----ITKPERVVGVIGASGSSVIMVAILRLEKI 174
QY 132 IVLCYGASSPALSDRKRFPTLFRTHPSATVHNPTRLKMKKFGWSRVAIL-----QQA 184
DQ 175 POISYASTAPDLSDNSRYDFFRVSPVSDTYQQAQMYDIVRKALKWNTVSTLASESGYGESG 234
QY 185 EEVFTSTVEDLENRCMEAGVEIVTRQSFSLSDPTDPAVNRLLRRODARIIVGLFYVVAARVYL 244
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Db 235 VEAFIQKRENGVCIQAQSVKIPREPKTGFEDKIIKRLLTSSNARGIIIFANEDDIRVL 294
Qy 245 CEMYQOYLGRAHVFFIGWEDNW-----YEVNLKAG-ITCIVEQMRIAAEGHLTT 296
Db 295 EAARANQTHG---PFWMG--SDSWGSKSAPVLRLEEVAEGAVTILPKRMSVRGFDYFS 349
Qy 297 EALMNQNNQTTISGTAEEFRRHLNQAIECYDI---NHDRYPE--GYQE---APLA 347
Db 350 SRTLDNRRNIWAFWEDNFCKLSRHALKGSHIKKTNRRERICQDSAYEGKGQVF 409
Qy 348 YDAVMSVALAFNKTMERLTGKSLRDFYTKKEIADEIYAAMNSQFGLVSG-VVAFSS 406
Db 410 IDAVYMGHALHAMHRLDPCRGVL--CPRMDPVDGTQLLKYYRNVSFGIAGNPVTFNE 467
Qy 407 QGDRIALQIEQIDMKYKEKLYDQDLN-----LSW-----LNTEQWIGKVP 451
Db 468 NGD-----APGRYD---IYQQLRNGSAEYKVGISWTDLHLRLIERMQWPGSGQ 514
Qy 452 QDRTIVT-----HVLRT----- 463
Db 515 LPRISCLPQCPGERKTKVGMACCWHCEPCTGYQYQVDRYTCCTCPYDMRPTENRTSQ 574
Qy 464 -----VSLPFCVCMCTISSGIFVAFALIIENWNKRRVIOSSHVPVCNTIM 510
Db 575 PPIPVKLEWDSWAVLPFLAVVGIAT-LFVVVTFVRYN----DTPIVKASGRELISYVL 629
Qy 511 LFGVIICLSVILLGIDGRFVSPEEPKPKICQARAWLLSTGFTLAYGAMFSKVRVHRFTT 570
Db 630 LAGIFLCVATTFLM-----IAEPD--LGTCSLRRIFGLGMSISYAALLTKTRIYRIFE 682
Qy 571 KAK--TDPKPKYEPKLYTWVSGLLSIDLVILLSQIFDPQRYLRYLETFPLEDPVSTDDI 628
Db 683 QGKRSVSAFRFSPASQALAITILISLQLLGICVWFVDPFSHVD---PQD--QRTLD 737
Qy 629 KIRPLEHCEQSNMGLVYGEKGLILVEGLFLAVETRISIKVKQINDSRVYVGMSTYV 688
Db 738 RFAPGVLKCDI--SLSLCLLGYSMLLWTCVYAIKTRGVP-ETFNEAKPIGFTMYTT 794
Qy 689 VVLCITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMILLIFVPKVIEWIRHPKDK 743
Db 795 CIVWLAFTPI--FFGTSQSADKLIYQTTTLTVSVLSASVSLGMLYMPKYVILFHEQN 852
Qy 744 AESKNPDASAISKEDEERYQKLVITENEQRLITQK 779
Db 853 VPKR-----KRSLKAVVTAATMSNKTQK 876

RESULT 10
MGR8_MOUSE STANDARD; PRT; 908 AA.
AC P47743;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPRC1H OR MGLUR8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=95239344; PubMed=7722646;
RA Duvoisin R.M., Zhang C., Ramonell K.;
RT "A novel metabotropic glutamate receptor expressed in the retina and
RL olfactory bulb.";
RL J. Neurosci. 15:3075-3083(1995).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB,
```

```
CC ACCESSORY OLFACTORY BULB, AND MAMMARY BODY. WEAKER EXPRESSION
CC IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDBRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17252; AAA68149.1; -.
DR GDB; GCR_1712; -.
DR MGD; MGI:1351345; Gprclh.
DR InterPro; IPR001828; ANF_Receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01058; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECP_F3_4; 1.
DR PROSITE; PS02059; G_PROTEIN_RECP_F3_4; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 565 565 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 908 AA; 101413 MW; 4CDD9D35827ED41F CRC64;

Query Match 8.1%; Score 355; DB 1; Length 908;
Best Local Similarity 21.0%; Pred. No. 3.6e-19;
Matches 200; Conservative 159; Mismatches 390; Indels 204; Gaps 44;

Qy 13 FWIFLCLIIASPHLOGGVAG-RPD-ELHIGGIFFIAGKGGWGOAC-----MP 59
Db 22 YWI--LTMQTHSQEYAHSLRDGDIILGGLFPVHAKG--ERGVPCGDLKKEGIHRL 77
Qy 60 ATRLALDDVNKQPNLLPGFKL---IL-----HSNDSCEPGL 93
Db 78 AMLVAIDQTKNDPDLNLTGLVRILDTCSRDTYALEQSLTFVQALIEKSDVRCANGD 137
Qy 94 GASVYNLLYNKPKQL--MLLAGCSTVCTTVAEAKMMNLIVLCYGASSPALSKRRPFT 151
Db 138 PP-----IFTKPKDISGVIGAAASSVIMVANILRLFKIPQISYASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVNPTRIKLMKKEGHSRVALQAAEEVFISTVEDLENRCHE-AGVEIVTRQ 210
Db 192 FSRVVPDSYQAQAMVDIVTALGNVYSTLASSEGNVSGEVGAFTQISRIGGVCIQAQSQ 251
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Db 24 LLLCALAAAAAGQEMYPHSHIRTEGDTV-----LGLPFPVHAKG--PSGVPCGDIKREN 74
QY 58 ----MPATRLALDDVKNQKNLLPGFKL---IL-----HSNDS 87
Db 75 GTHREAFMLYALDQINSDDNPNVTLGARITLTCSDRYALBQSLTFVQALIKQDTSV 134
QY 88 ECEPGLGASVMYLLNYPKQKMLLAGC--STVCTTVAEAAKMNVLVLCYGASSPALS 145
Db 135 RCTNTEPP-----VFVKPEKVGIVGASGSSVSIWVANILRLFPQIPQISYASTAPELS 188
QY 146 RKRFTPLFTHPSATVHNTPRIKLMKFKGSRVAILLQQAEEVFISVVEDLENRCMEAGV 205
Db 189 DRRYDFESRVPPDSFQAQAVDIVKALGN-----YVSLAS-EGSYGKGV 236
QY 206 IVTRGSFLSDPTDAVNLR-----RQDA-----RIIVGLFVVVAARRVLC-----EMYKQQL 252
Db 237 SFTQISKEAGGLCIAQSVIRPQERKDRITDFDRIIKQLIDTPNSRAVVFANDEIDIKQIL 296
QY 253 YG--RA-HWFFFIWYEDNW-----YEVNKAEGITCTVEOMRTAAEG---HLTEAL 299
Db 297 AAKRADQVGHFLWGSWSGSKINPLHQHEDIAEG-AITIQPKRATVEGDFAYFTSRTL 355
QY 300 -----MW-----NONNOTTISGMTAEF--RHRLNOALIEGYDINHDPYEGYQEP 345
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKKEDTRKCTGQERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVMSVALAFNPKMERLTT-----GKSLRDFTYTDKETADEIYAAAMS 392
Db 410 FVIDAYAMAHALHMHMKDLCADYRGVCPMEQAGGKLLK-----YIRN 454
QY 393 TOFLGVSQV-VAFSSQGDRIALTOIQMDGKYKLYGYDTQDLNLSW-----L 440
Db 455 VNFNGSAGTPVMFNKNG-----APGRYDIFQYQYTTNSNGRYLIGOWTDELQ 504
QY 441 NFE--QWIGG--KVP-----TDPKKVPEWPKLYTWSGLSIDLVILLSWQIEDPLQRYL 613
Db 505 NLEDQWQGVREIPASVCTLPCKPQQRKTKGTCCWTCPCDGVQYQFDEMTQCHP 564
QY 452 -----QDRIVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIIIFNIWNKHR 496
Db 565 YQDPNENRTGCODIPIKLEWSPWAV-IPVFLAMLGLIAT-IFVMATFIRYN----DT 618
QY 497 RVIOSSHPVCNTIMLFGVILICLISVILLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYG 556
Db 619 PIVRASGRLSVYLLTGIFLCYITIFLM-----IAKPD--VAVCSFRFVFLGLGMCISYA 671
QY 557 AMFSKVRVRRHTTKAK-----TDPKKVPEWPKLYTWSGLSIDLVILLSWQIEDPLQRYL 613
Db 672 ALLTKNRIYRFEQCKKSVTAP-RLISPTSQALITSSLSVQLLVFVWFGVDPNII 730
QY 614 ETPLEDPVSTDDIKIRPELECHESQORSNMWGLVYGFKGLILVFLGLFLAYETRSIKVK 673
Db 731 D-----YDEHKTNPQARGVLK-CDITDLQICSL--GYSILLMVTCTVVAIKTRGVP-E 782
QY 674 QINDSRVCMGSIYNNVVLGLITAPGVWGTASQODASFAV-----ALAVIFCFLSMLLI 728
Db 783 NFNEAKPIGFTYTTICVWLAFIPI--FFGTAQSAEKLYIQTTLTISMNLSASVALGML 840
QY 729 FVPKVIETIRHPKDKAESYNPDSALSKEDEERYQKLVTENEQQLRLITQKEEKIRVLQ 788
Db 841 YMPKVIIIFHPELNVQKR-----KRSFKAVVTAAWTSSRLSHKPSDR----- 883
QY 789 RLVERGDAGTEL 801
Db 884 ---PNGEAK-TEL 892
RESULT 12
MGR4_HUMAN
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96346635; PubMed=8738157;
RA Makoff A., Lelchuk R., Ower M., Harrington K., Emson P.;
RT "Molecular characterization and localization of human metabotropic
RL glutamate receptor type 4.";
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rostock P.R. Jr., Johnson B.G., Schoepf D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RL pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95342351; PubMed=7617140;
RA Flor P.J., Lukic S., Rueegg D., Leonhardt T., Knoepfel T., Kuhn R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RL 4.";
RL Neuropharmacology 34:149-155(1995).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X80818; CAA56784.1; -;
CC EMBL; U92457; AAB51762.1; -;
CC GCRDB; GCR_1891; -;
CC GCRDB; GCR_2069; -;
CC MIM; 604100; -;
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR01054; MTABOTROPICR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 610 I (POTENTIAL).

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FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 912 AA; 101867 MW; 4A2F36G3A2EAF5A CRC64;

Query Match 8.1%; Score 353; DB 1; Length 912;
Best Local Similarity 18.5%; Pred. No. 5.2e-19;
Matches 169; Conservative 179; Mismatches 371; Indels 196; Gaps 38;

QY 13 FWIFL-LCLTAS-----PHLQGGVAGRP-----DELHIGGIFPIAGKGGWGGQAC 57
Db 10 WVARLPCLLLSLXGPMPSLGRPKGPHMNSIRIDGDIITGLGFPVHGRG--SEGKPC 67
QY 58 -----MPATRLALDVNQPNLLPGFKL-----IL 82
Db 68 GELKKERGIHRLAMFLALDRINDPDLNITLGLARIDTCSDRTHALEQSLTFVQALI 127
QY 83 HSNDSECEPGLGASVMYLLNKKPKMLLAGC--STVCTTVAEAAKWNLVLCVGASS 140
Db 128 EKDTEVRCGGGPP-----IITKPERVGVGASGVSSVMVANILRFPKIPDISYASFA 183
QY 141 PALSDDRKRFPFLRTHPSVHNTPRIKMKKFGSRVAIL-----QOAEVEFSTIVE 193
Db 184 PLSDSNRYDFFSRVPSDTYQOAMVDIVRAALKWNYSTVASESGSYGESGVEAFQKSR 243
QY 194 DLENRCMEAGVEIVTROSFLSDPTDAVRN--LRQDARIIVGLFYVAARRVLCENYKQOL 252
Db 244 EDGVCVIAQSVKI--PREPKAGEFKIIRRLLETSNARAVIIPANEDDIRRVEAARRAQ 302
QY 253 YGRAHVFFIGWYEDNW-----YEVNLKAEG-ITCIVEQMRIAEAGHLTTEALMWNQN 304
Db 303 TGH---PFWMG--SDSMGSKTAPVLHLEEVAEGAVTILPKRMSVRGFDYFSRSLDNNR 357
QY 305 NQTTISGMTAEFRHRLNOALIEGYDI---NHDTYPE--GYOE--APLAYDAVWSVA 355
Db 358 RNIWFAEFWEDNFCKLSRHALKGSHVKCTNRERICQDSAYEGKGVQFVIDAVIANG 417
QY 356 LAFNKTMERLTGKSLRDTFTYDKETAIDEIYAAMNSTQFGLVSG--VVAFFSQGD---RI 411
Db 418 HALHAMRDLCPRVGL--CFRMPVDGTQLLKLYRNVSFIAGNPVTENGADPGRY 475
QY 412 ALQIEQID--GKYEKLG----YDTQLDNLSWLTQEWIGKV-----PODR-----454
Db 476 DIYQYQLRNSAEYKVGISWTDHLHLRIERMHPWPGSGQLPRSGICSLPCQGERKKTGK 535
QY 455 -----TIVTHVLRT-----VSPLPLFVC 471
Db 536 MPCCWHCEPCTGYQYDRTYCKTCPYDMRPTENTGCRPIPIIKLEWSPWAVLPFLFA 595
QY 472 MCTISSCGIFVAFALIIIFNIWKNHRRVIOSSHVPVNTIMLFGVILCLISVILLGIDGREV 531
Db 596 VVGLAAR-LFWVITFVRN-----DTPIVKASGRELSYVILLAGIFCYATTFLM-----IA 645
QY 532 SPEEYPKICQARAWLLSTGFTLAYGAMFSKVMRVRHRTTKAK--TDPKKKVEPKWLYTMV 589
Db 646 EPD--LQTCSLRRRIFLGLGMSISYAALLTKNRIYRIFEOGKRVSAPREFISPASQLAIT 703
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QY 590 SGLSIDLVILLSWQIFDPLQRYLETPEPVDSTDDIKIRPELEHCEORSNWMGLCLV 649
Db 704 FSLISLQLLGICVWFVVDPSHSVVD--FQD--QRTLPREFARGVLKCDI--SDLSLCL 756
QY 650 YGFKGLLTVFLGLFLAYETRSIKVKQINDSRVVGMSIYNVVLCLITAPVGMVIAQQDAS 709
Db 757 LGYSMLLMVTCVYVAIKTRGVP-ETFNKAKPIGFTMYTCIVWLAFTPI--FFGTSQSD 813
QY 710 FAFV-----ALAVIFCCFLSMLLIFVPKIEVIRHPKABSKYKNPDSAISKEDEERYQK 764
Db 814 KLIYQTTTLTVSVLSASVSGLMYPKVYIILFHPQNVPKR-----KRSLK 861
QY 765 LVTENEOLQRLITOK 779
Db 862 AVVTAATMSNKFQK 876

RESULT 13
MGR7_RAT ID MGR7_RAT STANDARD; PRT; 915 AA.
AC P35400;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
GN GRM7 OR GPRC1G OR MGLUR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=94117433; PubMed=828585;
RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
RA Mizuno N., Nakanishi S.;
RT "Molecular characterization of a new metabotropic glutamate receptor
RL mGluR7 coupled to inhibitory cyclic AMP signal transduction.";
RN J. Biol. Chem. 269:1231-1236(1994).
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=olfactory bulb;
RX MEDLINE=941195260; PubMed=8145723;
RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of a new member of the L-2-amino-4-
RT phosphonobutyric acid-sensitive class of metabotropic glutamate
RL receptors.";
RL Mol. Pharmacol. 45:367-372(1994).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC
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CC
CC EMBL; D16817; BAA04092.1; -.
CC EMBL; U06832; AAA20655.1; -.
CC GCRDB; GCR_0945; -.
CC GCRDB; GCR_0946; -.
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
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DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01057; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 591 615 I (POTENTIAL).
FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 628 648 II (POTENTIAL).
FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 675 III (POTENTIAL).
FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 703 723 IV (POTENTIAL).
FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 754 775 V (POTENTIAL).
FT DOMAIN 776 788 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 789 810 VI (POTENTIAL).
FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 826 850 VII (POTENTIAL).
FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 486 486 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 915 AA; 102231 MW; F28AFC4C6454A6C2 CRC64;

Query Match 8.1%; Score 353; DB 1; Length 915;
Best Local Similarity 21.2%; Pred. No. 5.2e-19;
Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LCLIA-----SPH-----LQGGVAGRPDELHIGGIFPIAGKGGWGGQAC----- 57
DB 24 LCLVIAAARGOEMTAPHIRIEGVDY-----LGGLPFVHAKG--PSGVPCGDIKREN 74
QY 58 ----MPATRLALDDVKNLPLGFKL-----IL-----HSNDS 87
DB 75 GTHRLEMLYALDQNSDNLNPNLTGLARILDTCSRDTYALEQSLTFVQALLQKDTSDV 134
QY 88 ECEPGIGASVMTNLYNKPQKMLLAGC---STVCTTVAEAKMNMNVLVLCYGASSPALSD 145
DB 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVSMVANILRLFPQISYASTAPELSD 188
QY 146 RKRFTPLRTHPSATVHNTRIKLKKFGWSRVAILQOAEVFPISVDELENRCMEAGVE 205
DB 189 DRYDFRSRVPPDSFQAQAMVDIVKALGN-----YVSTLAS-EGSYGKGV 236
QY 206 IYTRQSFSDPTDAVNRNL-----RODA-----RIIVGLFVVAARRVLC-----EMTKQOL 252
DB 237 SFTQISKEAGGLCIAQSVRIPOERKDRITDFRIKQLDTPNSRAVVFANDEDIKQIL 296
QY 253 YG--RA-HWFFIGWYEDNN-----YEVNLKAEGITCTVEOMRIAAEG---HLTAEAL 299
DB 297 AAKRAQDQVGHFLWVGSDSGSKNPLHQHEDIAEG-AITIQPKRATVEGFDAYFTSRTL 355
QY 300 -----MW-----NONQTTISGMTAEF-RHRLNQALIEGYDINHDPYEGVQEP 345
DB 356 ENNRNVVFAEYWEENFNKLTISGSKEDTRKCKQERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVWSVALAFNKTMTERTLT-----GKKSILRDPITYDKETADEIYAAMNS 392
DB 410 FVIDAVYAMAHALHNMKDLCDARYGVCPDMEQAGKLLKYIRHYN----- 456
QY 393 TQFLGVSGV-VAFSSQGDRIALTQIBQMDIGKYEKLGYYDTQLDNLSW-----L 440
DB 457 --FNSAGTTPVMFNKGD-----APGRYDIFQYQTTNTNPGYRLIGQWDELQ 504

QY 441 NTE--QWIGG--KVQP-----DRTIVTH-- 459
DB 505 NIEDMQGKGVREIPSSVCTLPCKPGQKTKTKGTPCWTCEPCDGYQYQFDEMTQCHCP 564
QY 460 -----VLR-----VSLPLFVCMCTISSCGIFVAFALIFINWKKRR 497
DB 565 YDQRPENRTGCONIPIIKLEHSPWAVIPVFLAMLGIAT-IFVMATFIRN-----DTP 619
QY 498 VIOSSHPVCMTIFLFGVILCLISVILLIGDGRFVSPEYPKICQARAWLLSTGFTLAYGA 557
DB 620 IVRASGRELVSLLTGIFLCYITFLM-----IAKPD--VAVCSFRFVFLGLGMCISYAA 672
QY 558 MFSKWRVHFTTKAK---TDPKKKVPKLYTMVSGLLSIDLVILLSWQIFDLPQRYLE 614
DB 673 LLTKNRIYRIFEGQKKSVTAP-RLISPTQSALITSSLSVQLLGVIFWGVDPNIIID 731
QY 615 TFPLEDVSTDDIKIRPELEHCESSQRNMMGLVYFGKGLILVFLGLFAYETRSIKVKQ 674
DB 732 ----YDEHKTMNPEQARGVLK-CDITDLQIICSL--GVSIILLMVTCTVYAIKTRGVP-EN 783
QY 675 INDSRYVGMISYNNVVLCLITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLI 729
DB 784 FNEAKPIGFTMYTTCIVMLAFIPI--EFGTAQSAEKLYIQTTTIFSMNLSASVALGMLY 841
QY 730 VPKVIEVIRHPKDKAESKYNPDSAISKEDEERYOKLVTENEQLRLITQKEEKIRVLQR 789
DB 842 MPKVIIFIRPELNVQRR-----KRSFRAVVTATMTSSRLSHKPSDR----- 883
QY 790 LVERGDAKGTTEL 801
DB 884 --PNGEAK-TEL 892

RESULT 14
MGR6_RAT STANDARD; PRT; 871 AA.
AC P35349;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR GPRC1F OR MGLUR6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=101116;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Retina;
RX MEDLINE=93280152; PubMed=8389366;
RA Nakajima Y., Iwakabe H., Akazawa C., Nawa H., Shigemoto R.,
RA Nakanishi S.;
RT "Molecular characterization of a novel retinal metabotropic glutamate
receptor mGluR6 with a high agonist selectivity for L-2-amino-4-
phosphonobutyrate";
RL J. Biol. Chem. 268:11868-11873(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR
LAYER OF THE RETINA.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).

DR EMBL: D13963; BAA03066.1; -.
DR PIR: A46742; A46742.
DR GCRdb; GCR_0623; -.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm.3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PRINTS; PR00593; MTABOTROPIC.
DR PRINTS; PR01056; MTABOTROPIC6.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
FT SIGNAL 1 18
FT CHAIN 19 871
FT DOMAIN 19 579
FT TRANSMEM 580 602
FT DOMAIN 603 616
FT TRANSMEM 617 637
FT DOMAIN 638 648
FT TRANSMEM 649 667
FT DOMAIN 668 691
FT TRANSMEM 692 712
FT DOMAIN 713 742
FT TRANSMEM 743 764
FT DOMAIN 765 777
FT TRANSMEM 778 800
FT DOMAIN 801 813
FT TRANSMEM 814 839
FT DOMAIN 840 871
FT CARBOHYD 290 290
FT CARBOHYD 445 445
FT CARBOHYD 473 473
FT CARBOHYD 561 561
SQ SEQUENCE 871 AA; 95089 MW; 9F70B4D6A13B186D CRC64;

Query Match 7.6%; Score 334.5; DB 1; Length 871;
Best Local Similarity 20.3%; Pred. No. 1.3e-17;
Matches 180; Conservative 150; Mismatches 350; Indels 199; Gaps 39;

QY 11 VTWIF---LCLTASPHLOGVAGRDELHIGGIFPIAGKGGWGOAC-----57
DB 11 LAWLISAGIACGAGSVRLGG-----LTGLGFPVHARGA--AGRACGALKKEQGVH 61

QY 58 -MPATRIALDDVNKPNLLPGFKLILHNSDECE-----PGLGA 95
DB 62 RLEAMLYALDRVNDPELLPGVRLGARLLDT-CSDRTYALQALSFVQALINGRGDGEA 120

QY 96 SV-----MYNLLYNKPKMLLAG--CSTVCTTVAEAKMNLIVLCYGASSPALSDRRK 148
DB 121 SVRCPGVPPLRSAPPRVAVVAVGASASSVIMVANVRLFAIPQISYASTAPELSDSTR 180

QY 149 FPTLFRTHPSATVNPRIRIKMKFGSRVAIL-----QQAEEVFSTVEDLENRME 201
DB 181 YDFSFRVVPDPSYQAQAVDVIIRALGNVYSTLASSENGYSGSEAFVQISREAGGVIA 240

QY 202 AGVEIVTRQFLSDPTDAVRNLR---QDARIIVGLFVYVAARVLCMEYKQOLYGRAH 257
DB 241 QSKIPREPQ---PGFHKVIRRLMETPNARGIIFANEDDIRVLBATQANUTGH-- 294

QY 258 VWFFIGWYEDNWE-----VNLKAEGL-TCTVEQMRTAAEG---HLTTEALMWNONOTT 308
DB 295 -FLWVG--SDSGWSKISPILNLEEAVGAILPKRASIDGFDQYFMRSL--ENNRRN 348

QY 309 ISGMTAEFRHLNQALIEGYD-----INHDYRPGYQAPLAYDAVWSVA 355
DB 349 I--WFAEFWEENFNCKLTSSGGQDDSTRKCTGEEIRGQDSAYEQEGKVQFVIDAVYA 406

QY 356 LAFNKYMERLTGKSL-ROFTYTDKELADEIYAAMNSTQFLVSGV-VAFSSQGD---R 410

DB 407 HALHSHQALCPGHTGLCPAMEPTD---GRTLHYINAVRFGNSAGTPVFNENGADPGR 463
QY 411 IALTQIE---QMIDGKYERLGY--DTQLDNLNLSWLNTEQWIGG--KVPQDRIV----- 457
DB 464 YDIFQYQATNGSSASSGGYQAVGQWAEALRD---MEVLRWSDGPHVPPSQCSLPCGPG 519
QY 458 -----THVLR-TVLSPL 468
DB 520 ERKKMKVGPCCWHCEACDGYRFQVDEFTCEACPGDMRPTPNHGTGRPTPVRLTWSSPW 579
QY 469 FVCMCTISSCGIFVAFALIIFNWNKRRVIOSSHPCVNTIMLFGV-IICLISVILLGID 527
DB 580 AALPLLLAVLIGMATTTIMATFMRHNDTPIVRASGRSLSYLLTGFLIYAITFLMVA-- 637
QY 528 GREVSPPEYPKICOARAWLLSTGTTLAYGAMFSKVRVHRFTTAK--TDPKKKVEPWKL 585
DB 638 -----EPCAAICAARLLGLGTLTSYALLTKTRIYRIFEQGRSVTPPPFISPTSQ 691
QY 586 YTMVSGLLSDILVILLSWQIFDPLQRYLETFFPLEDDIKIRPELEHCESQRNSMW 645
DB 692 LVITEGLTSLQVVGVIWLGQAQPHSVID---YEQRTVDPEQARGVLK-CDMSDLSL- 745
QY 646 LGLVYGFKGLILVGLFLAYETRSIKVKQINDSRYVMSIYNVVVLCITAPVGMVIA 705
DB 746 IGCL-GYSLLLMVTCTVYAIKARGVP-ETFEAKPIGFTMYTTCIIWLAFVPI--PFGTA 801
QY 706 QDASFVAVF---ALAVIFCCFLSMLLIFVPKVIEWIRHPKDAESK 747
DB 802 QSAEKIYIOTTLTVLSLSASVGLMYVPKTYVILFHPQNVQKR 848

RESULT 15
ID MGR3_RAT STANDARD; PRT; 879 AA.
AC P31422;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
GN GRM3 OR GPRC1C OR MGLUR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,
CC DENTATE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR2.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M92076; -; NOT_ANNOTATED_CDS.
DR PIR: JH0562; JH0562.
DR GCRdb; GCR_0362; -.

DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR003337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PRINTS: PR01053; MTABOTROPICR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 879
FT DOMAIN 23 576
FT TRANSMEM 577 599
FT DOMAIN 600 613
FT TRANSMEM 614 634
FT DOMAIN 635 645
FT TRANSMEM 646 664
FT DOMAIN 665 688
FT TRANSMEM 689 709
FT DOMAIN 710 734
FT TRANSMEM 735 756
FT DOMAIN 757 769
FT TRANSMEM 770 792
FT DOMAIN 793 802
FT TRANSMEM 803 828
FT DOMAIN 829 879
FT CARBOHYD 209 209
FT CARBOHYD 292 292
FT CARBOHYD 414 414
FT CARBOHYD 439 439
SQ SEQUENCE 879 AA; 98959 MW; 3E5965EDD5E6DEED CRC64;

Query Match 7.6%; Score 333; DB 1; Length 879;
Best Local Similarity 20.6%; Pred. No. 1.7e-17;
Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

QY 36 ELHIGGIFPIAGKGGQGC-----MPATRALDDVKNOPNLLPGFKLIHS 84
DB 38 DLVGLGLFPINERG--TGTECGRINEDRGIQLEAMLFADINKDNYLLPGVKLGVI 95
QY 85 NDS-----ECPGLGASVMYLLYNKPKMLLAGC-- 115
DB 96 LITCSRDYALQSLEFVRASLTKKVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147
QY 116 ----STVCTTVAEAKMNNILVLCYGSPALSDRKRPFTLFRTHPSATVHNPTRIKLMKK 172
DB 148 GSYSSVSIGVANLLRLFPQISYASTSAKLSKSDYDVFARTVPPDFYQAKAMAEILRF 207
QY 173 FGSRSVAIIQQAAEEVFISTVEDLE-----NRQMEAGVEIVTQSFSLDPTDAVRN-LRR 225
DB 208 FNTYVSTVASEGDYGETGIEAFQEARLNICI-ATAEKVGRSNIRKSYDSVIRELLQK 266
QY 226 ODARIIVGLF-----YVVAARRVLCYKQOYGRAHVWFEEIGWYEDNNWYEVNKA 277
DB 267 PNARVVV-LFMRSDSDSRELIANAARV-----NASPTWV-----ASDGGW----AQE 307
QY 278 GITCTVEQMRIAAGHLTTTEAL-----MWNQNNOTTIS 310
DB 308 SI--VKGSEHYVAGAITLELASHPVQRDPRYFQSLNPNYNNHRNPWFRDFWEQKFCQSLQ 364
QY 311 GMTAEFRHLNQALETGYDINHDPYEGYQAPLAY--DAYMSVALAFNKTMRLETTG 368
DB 365 -----NKRNRQVCKHLAIDSNEY---QESKIMFVVNAVYAMAHALKMQRTLCPN 414
QY 369 KKSRLDF--TYTDKEIADRIYAMNSTQFL----GVSGVVAFSSQGDRIALTQI--BQMI 420
DB 415 TTCLCDAMKILDGKLYKEYLLKINFTAPFPNPNKGADSIYKFDFTFGDGMGRYVFNLOQT 474

QY 421 DGKYE--KLGYY----DTQLDNLSSW-----LATEQ-----WI----- 446
DB 475 GGYSLYLVGHWAETLSLDVDSIHWSRNSVPTSOCSDDCAPNEMKNMQPGDVCCWICIPC 534
QY 447 -----GKVP-----QDRTIIVTHVLTVSPLFVCMC 473
DB 535 EPEYLVDEFTCMDCGPGQWFTADLSGCYNLPEDYIKWEDAWAIGPV--TIACLGFLCTC 592
QY 474 TISSCGIFVAFALIFINWKNHRR---VIOSSHVPVCNTIMLFGYIICLIISVILLGIDGRF 530
DB 593 -----IVITVFIKHNTPLVKASGRELC-YILLFGVSLSYCMTF-----F 631
QY 531 VSPREYPKICOARAWILLSTGFTLAYGAMFSKVRVHRTTAKTDPK--KKVEPKLYTM 588
DB 632 FIAKPSPVICALRRLGLGTSFAICYALLTKNCIARIFDGVKNGAQRPKFISPSQVFI 691
QY 589 VSGLLSLDLVILLSSQWIFDP--LQRYLETFFLEDVSTDDIKIRPELEHESORNSMWL 646
DB 692 CLGLILQIVMVSVMWLIETPTTRY--TLP-----EKRETIVILKCNVDSSMLI 739
QY 647 GLVYGFKGLILVFGFLAYETRSIKVKQINDSRVYVGMISYVNVVLCITAPVGMVIA 706
DB 740 SLTYDV--VLVILCTVYVAFKTRKCP-ENFNEAKFIFGTMYTTCIIWLAFLEFIFYVTSSDY 796
QY 707 DASFAFVALAVIFCCFLSMLLIFFVPKVIEVIRHFK 741
DB 797 RVQTTMCISVSLSGFVVVGLGFAPKVHIVLFOPQ 831

Search completed: April 30, 2002, 10:16:52
Job time: 224 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:12:33 ; Search time 32.13 Seconds
(without alignments)
3824.113 Million cell updates/sec

Title: US-09-715-962-2

Perfect score: 4374

Sequence: 1 MKDMSDGAFTVFIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4374	100.0	840	5 Q9BML7	Q9bml7 drosophila
2	3317	75.8	1713	5 Q9V309	Q9v309 drosophila
3	1746.5	39.9	816	5 Q9N502	Q9n502 caenorhabdi
4	1186.5	27.1	1220	5 Q9BML6	Q9bml6 drosophila
5	1183.5	27.1	1221	5 Q9Y133	Q9y133 drosophila
6	1022.5	23.4	1305	5 Q9VPS7	Q9vps7 drosophila
7	1018.5	23.3	1305	5 Q9BML5	Q9bml5 drosophila
8	457	10.4	402	5 Q23442	Q23442 caenorhabdi
9	362.5	8.3	976	5 Q9V485	Q9v485 drosophila
10	343.5	7.9	983	11 Q62916	Q62916 rattus norv
11	342	7.8	879	11 Q9QYS2	Q9qys2 mus musculu
12	334.5	7.6	528	5 Q96954	Q96954 geodia cydo
13	330	7.5	872	4 Q9H3N6	Q9h3n6 homo sapien
14	330	7.5	977	13 Q9PWE1	Q9pwe1 ictalurus p
15	299.5	6.8	1188	13 Q98UC5	Q98uc5 gallus gall
16	297.5	6.8	1242	13 Q98UC4	Q98uc4 gallus gall
17	294.5	6.7	1156	13 Q98UC6	Q98uc6 gallus gall
18	274.5	6.3	153	11 Q9QY85	Q9qy85 rattus norv
19	267	6.1	1199	11 Q9EPV6	Q9epv6 mus musculu

20	247.5	5.7	870	5 Q9N4T8	Q9n4t8 caenorhabdi
21	243.5	5.6	856	13 Q73638	Q73638 fugu rubrip
22	241.5	5.5	868	13 Q73636	Q73636 fugu rubrip
23	240	5.5	912	10 Q9C561	Q9c561 arabidopsis
24	237	5.4	877	13 Q9PW88	Q9pw88 carassius a
25	235	5.4	844	13 Q93552	Q93552 carassius a
26	231.5	5.3	738	5 Q9V4U3	Q9v4u3 drosophila
27	231.5	5.3	864	13 Q73637	Q73637 fugu rubrip
28	227	5.2	875	13 Q73640	Q73640 fugu rubrip
29	224.5	5.1	1056	13 Q9Y117	Q9y117 squalus aca
30	223	5.1	1055	13 Q9YGM3	Q9ygm3 oryzias lat
31	222	5.1	1055	13 Q98U11	Q98u11 oryzias lat
32	219.5	5.0	848	13 Q93553	Q93553 carassius a
33	219	5.0	941	10 Q9SWD9	Q9swd9 arabidopsis
34	212	4.8	1267	5 Q93564	Q93564 caenorhabdi
35	211.5	4.8	925	10 Q65498	Q65498 arabidopsis
36	211.5	4.8	962	10 Q23048	Q23048 arabidopsis
37	209	4.7	1070	13 Q93490	Q93490 anguilla ja
38	207	4.7	880	11 Q35190	Q35190 mus musculu
39	202.5	4.6	880	13 Q73639	Q73639 fugu rubrip
40	201.5	4.6	912	10 Q9SES5	Q9ses5 brassica na
41	195	4.5	843	11 Q9Z0R7	Q9z0r7 rattus norv
42	193.5	4.4	551	13 Q9PWQ0	Q9pwq0 fugu rubrip
43	190.5	4.4	923	10 Q9ZV68	Q9zv68 arabidopsis
44	189.5	4.3	953	10 Q9ZV67	Q9zv67 arabidopsis
45	187	4.3	502	13 Q98845	Q98845 anguilla ja

ALIGNMENTS

RESULT	1				
Q9BML7					
ID	Q9BML7	PRELIMINARY;	PRT;	840	AA.
AC	Q9BML7				
DT	01-JUN-2001 (Tremblrel. 17, Created)				
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)				
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)				
DE	METABOTROPIC GABA-B RECEPTOR SUBTYPE 1.				
GN	GABA-B-R1.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=11168554;				
RA	Mezler M., Muller T., Raming K.;				
RT	"Cloning and functional expression of GABA-B receptors from				
RT	Drosophila.";				
RL	Eur. J. Neurosci. 13:477-486(2001).				
DR	EMBL; AF318272; AAK13420.1; -.				
KW	Receptor.				
SQ	SEQUENCE 840 AA; 94384 MW; C091A9F406C97500 CRC64;				

Query Match 100.0%; Score 4374; DB 5; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRKDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHIGGIEPIAGKGGWGGQACMPA	60
DB	1	MRKDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHIGGIEPIAGKGGWGGQACMPA	60
QY	61	TRLALDDVKNQNLPGFKLILHSNDSECEPGLGASVMYNLLYNKPKMLLAGCSTVCT	120
DB	61	TRLALDDVKNQNLPGFKLILHSNDSECEPGLGASVMYNLLYNKPKMLLAGCSTVCT	120
QY	121	TVAEAAKMNLLIVLCYGASSPALSDRKRPFTTLFTRHPSATVHNPTRIKLMKFGWSRVAI	180
DB	121	TVAEAAKMNLLIVLCYGASSPALSDRKRPFTTLFTRHPSATVHNPTRIKLMKFGWSRVAI	180

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Qy 181 LQAAEEVFISTVEDLENRCMEAGVEIVTRQSFSDPTDAVRNLRRODARIIVGLFVVA 240
Db 181 LQAAEEVFISTVEDLENRCMEAGVEIVTRQSFSDPTDAVRNLRRODARIIVGLFVVA 240
Qy 241 RRVLCMYKQQLYGRAHVFFIIGWEDNNYEVNKLKAEITCTVCEQMRIRAAEGHLLTTEALM 300
Db 241 RRVLCMYKQQLYGRAHVFFIIGWEDNNYEVNKLKAEITCTVCEQMRIRAAEGHLLTTEALM 300
Qy 301 WNQNQTTISGMTAEFRHLRNLQALIEEGYDINHRYPEGYQAPLAYDAVMSVALAFNK 360
Db 301 WNQNQTTISGMTAEFRHLRNLQALIEEGYDINHRYPEGYQAPLAYDAVMSVALAFNK 360
Qy 361 THERLTTGKSLRDFTYTDKETADEIYAAMNSTQFLGSGVWAFSSQGRIRALTOEQMI 420
Db 361 THERLTTGKSLRDFTYTDKETADEIYAAMNSTQFLGSGVWAFSSQGRIRALTOEQMI 420
Qy 421 DGKYEKLGYYDQDLNLSWLNTQEWIGKGVPODRTTIVTHVLRVSLPLFCVCMCTISSCGI 480
Db 421 DGKYEKLGYYDQDLNLSWLNTQEWIGKGVPODRTTIVTHVLRVSLPLFCVCMCTISSCGI 480
Qy 481 FVAFALIIIFNIWKNRRVTOSSHPVCNTIMLFGVILCLISVILLGIDGRFVSPPEYPKIC 540
Db 481 FVAFALIIIFNIWKNRRVTOSSHPVCNTIMLFGVILCLISVILLGIDGRFVSPPEYPKIC 540
Qy 541 QARAWLLSGFTLAYGAMESKVMRVHRTTKAKTDPKKKVPEPKLYTMVSGLLSIDLVIL 600
Db 541 QARAWLLSGFTLAYGAMESKVMRVHRTTKAKTDPKKKVPEPKLYTMVSGLLSIDLVIL 600
Qy 601 LSWQIFDPLQRYLETFPLEDPDVTDDIKIRPELEHCESSQNSMVLGLVYGFGLIIVFG 660
Db 601 LSWQIFDPLQRYLETFPLEDPDVTDDIKIRPELEHCESSQNSMVLGLVYGFGLIIVFG 660
Qy 661 LFLAYETRSIKVKQINDSRVGMISYVNVVCLITAPVGMVIAQQDASFAFVALAVIFC 720
Db 661 LFLAYETRSIKVKQINDSRVGMISYVNVVCLITAPVGMVIAQQDASFAFVALAVIFC 720
Qy 721 CFLSMILLIFPVKVIEWIRHPKDKAESKYNPDSAISKEDEERYOKLTENBQLORLTQKE 780
Db 721 CFLSMILLIFPVKVIEWIRHPKDKAESKYNPDSAISKEDEERYOKLTENBQLORLTQKE 780
Qy 781 EKIRVLQRQLVERGDAKGFELNGATGASAAVATTQSPASLINSSAHATPAATLATTOGE 840
Db 781 EKIRVLQRQLVERGDAKGFELNGATGASAAVATTQSPASLINSSAHATPAATLATTOGE 840

RESULT 2
Qy 09V309 PRELIMINARY; PRT: 1713 AA.
AC Q9V309;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG15274 PROTEIN.
GN GABA-B-R1 OR BG:DS00929.6 OR CG15274.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Caden A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flocker A., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region."
RL Genetics 153:179-219(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RA Celniker S.E., Agbayani A., Arcalini T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003646; AAF53431.1; -
DR EMBL; AE003411; AAF44910.1; -
DR FlyBase; FBgn0028924; GABA-B-R1.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000402; Na_K_beta.
DR Pfam; PF000003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 2.
KW Hypothetical protein.
SQ SEQUENCE 1713 AA; 195133 MW; 8474EBC5F9FA27AC CRC64;
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Query Match 75.8%; Score 3317; DB 5; Length 1713;
Best Local Similarity 45.0%; Pred. No. 7.3e-251;
Matches 737; Conservative 16; Mismatches 19; Indels 866; Gaps 10;

Qy 3 KDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHGTGGIPPIAGKGGQGCMPATR 62
Db 142 RDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHGTGGIPPIAGKGGQGCMPAAR 201
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QY 63 LALDDVNKQPNLLPGFKLILHSNDSCEPGLGASVWYNLLYNKPKMLLACGCTVCTTV 122
Db 202 LALDDVNKQPNLLPGFKLILHSNDSCEPGLGASVWYNLLYNKPKMLLACGCTVCTTV 261
QY 123 AEAAMNLLIVLCYGASSPALSDRRFPTLRTHPSATVHNPTRIKLMKKFGWSRVAILQ 182
Db 262 AEAAMNLLIVLCYGASSPALSDRRFPTLRTHPSATVHNPTRIKLMKKFGWSRVAILQ 321
QY 183 QAEVFISTVEDLNRCEAGVEIVTQSFSDPTDPAVNRLLRQDARIIVGLFYVVAARR 242
Db 322 QAEVFISTVEDLNRCEAGVEIVTQSFSDPTDPAVNRLLRQDARIIVGLFYVVAARR 381
QY 243 VLCEMYKOQLYGRAHVWFFIGWYEDNWEVNLKABGICTVEQMRIAAEGHLLTTEALMN 302
Db 382 VLCEMYKOQLYGRAHVWFFIGWYEDNWEVNLKABGICTVEQMRIAAEGHLLTTEALMN 441
QY 303 QNNQTTISGMTABEF-----RRLNQALIEEGYDINHDPYEGY 341
Db 442 QNNQTTISGMTABEFRLVLLPLKFLLOCAFFLRRLNQALIEEGYDINHDPYEGY 501
QY 342 QEAPLAYDAVMSVALAFNKTMERLTTGKSLRDFTYTQKEIADETIYAAMNSTQFLGVSGV 401
Db 502 QEAPLAYDAVMSVALAFNKTMERLTTGKSLRDFTYTQKEIADETIYAAMNSTQFLGVSGV 561
QY 402 VAFSSQGDRIALTQIEQMIDGKYEKLGYYDTQDNLNLSWLNTEQWIGGK-----449
Db 562 VAFSSQGDRIALTQIEQMIDGKYEKLGYYDTQDNLNLSWLNTEQWIGGKTKHVTTPNKN 621
QY 450 -----449
Db 622 GNPSKDDVNRGSLTSLSEKNDESKNPSSASLOAPKVPKPKKLSISDAGKDTVTOKV 681
QY 450 -----449
Db 682 KENEPEGFSQFKESIGVRANRNSSATKENEKLLVTVPGKSLIKESNDENPEPSRRT 741
QY 450 -----449
Db 742 KSQPVGKVVYESSTRVRPEFDFDREKYLSDMIDYDRSDEDVPEKKLSWEPDSTLRRR 801
QY 450 -----VPO-----452
Db 802 FVSNNEYHSSLEGEEDLDSVGSSTMRGYSRMPQNAEDERPVLAEIINMGKLKELKE 861
QY 453 -----DRTI-----VTHV-----460
Db 862 QRESTNVRNRRDDKTIDEVYKSGKITGTSKQHVVEVKYNETASNEDDDNAQVKHIGTIT 921
QY 461 -----460
Db 922 KIFSIAQRMKEKSKSEEDENKDNKDKDKENKDEQKLPPPEIELEAKKAWTPTPI 981
QY 461 -----460
Db 982 AETSPDIPGENOILQEQYQVKIGKRNRYRCIGINTDISRKSKITFTSKSAGDDLVDVYH 1041
QY 461 -----LRTVSLPLFV-----470
Db 1042 DGGRLRDIGOTTENLKNQKNHKKHTEPDDIPVDIGHSDDRVREIGVNTKKLPKIIIPPI 1101
QY 471 -----470
Db 1102 AEMHVHNGKLRDGTGTDKPFWPIDGTDVIYHPIKTRDKKLNKLLVDPDPPDNGPYKM 1161
QY 471 -----C-----MCTISSCGIFVAFALII 488
Db 1162 PTKEDRTYVYKCEYHPGRTETWRRLPFENKIHGKYKLRPPSHWLYTVFSVLYILFVIIF 1221
QY 489 FNTW-----492
Db 1222 SMAWFDFIKDDASRKVPIMKAQPFISFTPIGPRTNPKAVSFDPRNSTEVMKYAGIMAL 1281
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QY 493 -----492
Db 1282 LEKYGDYGHNPFGTCTANEKFGYPSGEPVFLKVNRIIGFKTEPYINSDLYKAKIDEV 1341
QY 493 -----N 493
Db 1342 EFTALKRLLLENTTTEBGLNRTWITCRSDKDKNVLIEFHPPEPAIRTYTDIEEKIEYIAN 1401
QY 494 KHR-----VTQSSHPVCNTIMLFGVILICISVI 522
Db 1402 EGKKSFFGPNVNRIVALKIKNLKANERVHINCKIVIQSSHPCVNTIMLFGVILICISVI 1461
QY 523 LIGIDGRFVSPEYPKICQARAWLLSTGFTPLAYGAMFSKVMVRHRTTKAKTDPKKKVEP 582
Db 1462 LLGIDGRFVSPEYPK-----1477
QY 583 WKLYTWVSGLLSIDLLVILLSWQIFDPLQRYLETFFLEDPVSTTDDIKIRPELEHESQRN 642
Db 1478 -----IFDPLQRYLETFFLEDPVSTTDDIKIRPELEHESQRN 1515
QY 643 SMWLGIVYGFGLILVFLGFLAYETRSIKVKQINDSRVVGMSIYNVVLCLITAPVGMVI 702
Db 1516 SMWLGIVYGFGLILVFLGFLAYETRSIKVKQINDSRVVGMSIYNVVLCLITAPVGMVI 1575
QY 703 ASQODASFAFVALAVIFCCFLSMLLIFVPKIVIEVRHPKDKAESKYNPDSAISKEDEERY 762
Db 1576 ASQODASFAFVALAVIFCCFLSMLLIFVPKIVIEVRHPKDKAESKYNPDSAISKEDEERY 1635
QY 763 OKLVTNEQLORLITOKEEKIRVLRORLVERGDAKGTGELNGATGASAAVATTISQASLI 822
Db 1636 OKLVTNEQLORLITOKEEKIRVLRORLVERGDAKGTGELNGATGASAAVATTISQASLI 1695
QY 823 NSSAHATPAATLAIOTGE 840
Db 1696 NSSAHATPAATLAIOTGE 1713

RESULT 3
Q9N502 PRELIMINARY; PRT; 816 AA.
ID Q9N502;
AC Q9N502;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE Y41G9A.4 PROTEIN.
GN Y41G9A.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Ryan E., Wohlman P., Walker C., Fielder T.;
RT "The sequence of C. elegans cosmid Y41G9A.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006761; AAF60549.1; -.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
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DR Pfam; PF01094; ANF_receptor; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 816 AA; 92251 MW; 4363D1IA46CBECAL CRC64;

Query Match	39.9%;	Score 1746.5;	DB 5;	Length 816;
Best Local Similarity	46.4%;	Pred. No. 3.7e-128;		
Matches 356;	Conservative 131;	Mismatches 251;	Indels 29;	Gaps 11;

Qy	46	AGKGGWGGQACMPATRIALDDVKNQPNLLPGFKLIHLSNDSCEPGLGASVMYNLLYK	105
Db	3	SGSGWAGGAGACLPAVDMALKDVNSRLDILPGVYVLTNNTHNSQCQGLAMQQLYDFLYKP	62
Qy	106	PQKMLLAGCSTVCTTVAEAAKWNLLIVLYCIGASSPALSDDRKFPTLFRTHPSATVHNPT	165
Db	63	PTKMLLTGCSPTVTIAEAAPVWKLVLYSGSSPALSNNRNPFTLFRTHPSANMNPT	122
Qy	166	RIKLMKFGNSRVAILOQAEVFISTVDELENRCMAGVEIVTRQSFGLSDPTDAVNRLLR	225
Db	123	RIHIMEFKKRRFTILMSVEVPVFTAKDLEATARKGIK-VDRQSFYGDPTDAMKTLOR	181
Qy	226	QDARIIVGLFVYVAARRVLCEMYKQOLYGRAHWFFITGMVEDNMYEVNKLKAEIGITCVBQ	285
Db	182	QDARIIVGLFVTEARKVLCOAYHHGLYGRRYVWFITGMVADTWY-IPPEEHLNCTAQD	240
Qy	286	MRIAAEGHLTEALMWNQNOTTISGMTAEPRHRLNQALIEGSDIINHDRPPEGQEAP	345
Db	241	MTEAAEYHFTESVYMLSRDNIPIASEMTGMQFOURLTOYFQKDTANVG-----GFPEAP	294
Qy	346	LAYDAVMSVALAFNKTWERLTTGCKLSURDFTYTDKEIADIEYAAAMSTOFLGVSGVVAFS	405
Db	295	LAYDAVWALAFNCTRNNLPISHR-LENFTYDNKYIADTLFOCVANTSEFVSGVSGKWFMS	353
Qy	406	SQGDRIALTOEQMIDGKYEKLYGYDFQDLNLSWLNTEQWIGK-VPODRTIIVTHVLRTV	464
Db	354	DSGDRIARTQEQMQGKYKIMGYDFTSGDLEWYNKEQWLNGKPPDPSTVIKKHAMTV	413
Qy	465	SLPLFVCMCTISSCGIFVAFALIIFNILWNKHRRVIOSSHVCNTIMLFGVITCLISVILL	524
Db	414	SNEFYPTILFVUGIAACVFIYLTQKHHERUIIFQSQPECNNILIGCSLCLFLSLFI	473
Qy	525	GI--DGRFVSPDEEYPKICQARAWLLSTGFTLAYGAMFSKVMRVHRE--TTKAATDPKKV	580
Db	474	GLPSDDISISESLPPLCHARVITLLGFTTFAGSGMFAKVIIVHRMGATENQOLASRQKD	533
Qy	581	EP--WKKLYTMVSGLLSIDLIVLLSWOIFDPLQRYLETFPLEDPVSTDDIKIRPELEHC	637
Db	534	EPISSSFYVIVAALTADVDFVCFVWVLIDPLHLTEQKPLFTPADSEDEMIMPVQQC	593
Qy	638	ESQRNSWGLGLVYFGKGLILVFLGFLAYETRSIKVKQINDSRVYGMISINVVVLCILITAP	697
Db	594	OSNOQEVWIGLIMFGKCLLVFGFTFSYETRNKLKRFINDSRFVGLAIYNVAVMTLVATP	653
Qy	698	-VGMVIAQQDASPAFVALAIFCCFLSMLLIFVPKVIEWIRHPKDAESKNPD---SA	753
Db	654	VVTLIIHGKVDAEAFISLIV-----GLTYGPKIRHIKYPVPSADELQNLGNVPGV	705
Qy	754	ISKEDEERYOKLVNTENSOQLRITQKEEKIRVLRLQRLVERGDAGKTE	800
Db	706	MSKVDQKRYKMLKKNETLQIQIEKERKTHECKERKEELTKNSEET	752

RESULT	4	
Q9BML6		
ID	Q9BML6	PRELIMINARY; PRT; 1220 AA.
AC	Q9BML6;	
DT	01-JUN-2001	(TrEMBLrel. 17, Created)
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2001	(TrEMBLrel. 17, Last annotation update)
DE	METABOTROPIC GABA-B RECEPTOR SUBTYPE 2.	
GN	GABA-B-R2.	
OS	Drosophila melanogaster	(Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	

OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=727;
RN	[1]
RP	SEQUENCE FROM N. A.
RX	PubMed=11168554;
RA	Mezler M., Muller T., Raming K.;
RT	"Cloning and functional expression of GABA-B receptors from
RT	Drosophila.";
RL	Eur. J. Neurosci. 13:477-486(2001).
DR	EMBL; AF318273; AAK13421.1; -;
KW	Receptor.
SO	SEQUENCE 1220 AA; 137976 MW; 2B33DA2C1A18DA8B CRC64;

Query Match	27.1%;	Score 1186.5;	DB 5;	Length 1220;
Best Local Similarity	32.9%;	Pred. No. 5.8e-84;		
Matches 272; Conservative	183;	Mismatches 311;	Indels 61;	Gaps 23;

[illegible]

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Db 759 FRKALMEKENELQALIRKL---GPEARKWIDGVTCTGGSGNVGSELEP 802

RESULT 5
Q9V133 ID Q9V133 PRELIMINARY; PRT; 1221 AA.
AC Q9V133
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BCDA:GH07312 PROTEIN.
GN GABA-B-R2 OR BCDA:GH07312 OR CG6706.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levine S.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Moulton G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-F., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agbayani A., Arcania T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirskaas R.R., Weinburg T.,
RA Celniker S.E.
RT "Full length Drosophila melanogaster cDNA sequence."
RL Submitted (Apr-1999) to the EMBL/genBank/DBJ databases.
DR EMBL; AE003736; AAF55916.1;
DR EMBL; AF145639; AAD38614.1;
DR FlyBase; FBgn0027575; GABA-B-R2.

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DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 2.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 1221 AA; 138123 MW; A57A9954F31F0A05 CRC64;

Query Match 27.1%; Score 1183.5; DB 5; Length 1221;
Best Local Similarity 32.8%; Pred. No. 9.9e-84;
Matches 271; Conservative 184; Mismatches 311; Indels 61; Gaps 23;

QY 17 LLCLIASPHLQGGVAGRPDELHIGGIFPIA-GKGGWGGQACHPATPALDLDVKNQPNLL 75
DB 12 LFLLLWSTACGRKTAKRSD-VYIAGFFPYGDGVENSYTGKVMPSVKLALGHVNEHGKIL 70
QY 76 PGFKLILHSNDSCEPLGASVMYNNLLYNKPKMLML-AGCSTVCTTVAEAAKWNLIVL 134
DB 71 ANYRLHWNNDTQCNAAVGVKSFDDMHSGPNKVMLEGAACHTVTDPIAKASKHWHLTQL 130
QY 135 CYGASSPALSDRRKRPPTLFRTPHSATVHNPTRIKLMKFCWSRVAILQQAEEVFI---S 190
DB 131 SYADTHPMET-KDAFFNFRVVPVSENAFNAPRLALLKEFNWRTVGTVYQNEPRYSLPHNH 189
QY 191 TVEDLENRCWEAGVEIVTROSFLSDPTDAVRLNRQDARIIVGLFYVVAARRVCEMYKQ 250
DB 190 MVADLD--AME--VEVETQSFVNDVAESLKLREKDVRIILGNFNEHFARKACEAYKL 245
QY 251 OLYGRAHVWFFIGWYEDNWVEVNLKAGICTVEQMRIAEGHILTTALAMWNONNOTTIS 310
DB 246 DMVGRAYQLIMATYSTDMWNVTQDSE---CSVEETATALEGAILVDLLPLSTSGDITVA 302
QY 311 GMTAEFRRLNQAILEEYD---INHDRYPGQEPALAYDAVMSVALAFNKTWERILT 366
DB 303 GITADEY-----LYE--YDLRGTEYSRF-HGY-----TYDGIWAALALIOYVAEK-- 345
QY 367 TGKKSURDFTYTDKEIADEIYAAMNSTQFLGVSGWVAFSSQGDRIALTOEQMIDGKYEK 426
DB 346 -REDLLTHFDYRVKDWESVLEALRNTSPFEGVTGPVRFYN-NERKANILINQFOLGOMEK 403
QY 427 LGYDFTQLD--NLSWLNTFQWIGGKVPQDRTIYTHVLTYSPLFCVMCTISSCGIFVAF 484
DB 404 IGEYHSQKSHLDLSLGLKPKWVGKTPPKDRTLIYIEHSQVNTPTIYIVSASVIGVLIAT 463
QY 485 ALTIIFNKNHRRVIOSSHHPVCNTIMLFGVILICISVILIGIDGRFVSPEEYPKICOARA 544
DB 464 VFLAFNFKVRNQYIKMSSPHLNNLIIVGCMWYLSIIFLGLODTTLSSVAAPFYICTARA 523
QY 545 WLSTGFTLAYGAMFSKVRVVRHFTTKAKTDPPKKVPWKLYTMVSGLLSIDLVILLSWQ 604
DB 524 WILMAGFSLSGAMFSKTRVHSHFTDLKLN-KKVIKDYQLFMVVGVLAIADIAITWQ 582
QY 605 IDPLQRYLETFFLEDPV--STTDDDKIRPELEHCSQRNSMGLVYGFGLILVFGFLF 662
DB 583 IADPF--YRETKOLE-PLHENIDDDLVIPENEYCOSEHMTIFVSIITAYKGLLVFGAF 639
QY 663 LAYETSRIVKQINDSRVYCMYNNVVLCLITAPVGMVIAQQODASFAFVALVIFCCF 722
DB 640 LAWETRHVSIPALNDSKHIGFSYNNVFITCLAGAAISLVLSDRKDLVFLLSFFITFTT 699
QY 723 LSMILFVFPKIVIRHPKDKAESKNP-----DSAIKSEDEERYOKLVENEQ 771
DB 700 ATLCLVFPKLVKLKPNQGVVDKRVKRALRPMKNGRRDSSVC-ELEQRLRDVKNTNCR 758
QY 772 LQRLITQKEEKIRVLRQLRVERGDAKGTGLNGATGVASAAVATTSQP 818
DB 759 FRKALMEKENELQALIRKL---GPEARKWIDGVTCTGGSGNVGSELEP 802

RESULT 6
Q9VPS7 ID Q9VPS7 PRELIMINARY; PRT; 1305 AA.
AC Q9VPS7;

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RX PubMed=11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
RT Drosophila";
RL Eur. J. Neurosci. 13:477-486(2001).
KW EMBL; AF318274; AAK13422.1; -.
SQ SEQUENCE 1305 AA; 143701 MW; 8BBFA80F0E9BEADD CRC64;

Query Match 23.3%; Score 1018.5; DB 5; Length 1305;
Best Local Similarity 29.0%; Pred. No. 9.7e-71;
Matches 249; Conservative 171; Mismatches 349; Indels 91; Gaps 22;
QY 41 GIFFPIA-GKGWGQGOACQACATRIALDDVKNPOLLPGFKLILHNSDECEPLGASVMY 99
Db 157 GLFELSTSRGPRPDGLSELGAATMAVEHINRK-RLLPYTLVLTNDTQCDPGVGVDREF 215
QY 100 NLLYNKQKMLL---AGCSTVCTVABAAKWNILVLCYGASSPALSDRRKRFPLFRTH 156
Db 216 HAIYTOPSTRVMVLLGSACSEVTESLAKVWPYWNIVQVSFGSTSPALSDRRFPYFRTV 275
QY 157 PSATVHPNTRIKMKKGWSVAILQAAEEVFISTVEDLENRCMEAGVEIVTQSF-LSD 215
Db 276 APDSSHPNPAITAFIRKFGVGVTFTSQNEEVHSLAVNNLVTELEAANISCAATITFAATD 335
QY 216 PTDVARNLRRODARIIVGLFVVAARRVLCEMYKOOLYGRAHVWFF-----IGWIEDNMY 270
Db 336 FKEQLLLRETDTRIIGSFQELAPOLICEAYRLRMFGADYAWILHESMGAPWPD--- 392
QY 271 EVNLKASGITVQVPMIAAEGHITTEALMWNQNNQTTISGMTAEFFRHLNQALIE--- 327
Db 393 -----QRTACSNHELQLAVENTLIVVSTHNSIVGNVNSYSLGNHMHNSQLRKQSAQPHG 446
QY 328 -----EGY-----DINHRR-----YPEGY-QEAPLAYDAVWSVALAF 358
Db 447 ODGFGSGYGPRIATAQSDSRRRRRRRGVGTSGHLPFEPAISQYAPQYDAVWAIALAL 506
QY 359 NKTME--RLATGKSLRDTFTYDREIADEIYAAMNSTOFLGVSGVWAFSSOGDRIALQI 416
Db 507 RAAEHRNRNEEQKLGDFYTRSDMAWEFLQMGKHLFLGVSGVPSFGP-DRVGTAF 565
QY 417 EQMIDGKYELGYYDTQDNLNSW----LNTQWIGKGYPODRTIVTHVLRVSLPLFCYM 472
Db 566 YIQIGLLEPVALVYPATDALDFRCPRCPVKWHSQVPIAKRYFKLRVATIAFLAFYTI 625
QY 473 CTISSCGIFVAFALIININKNHRRVIOSSHPVNTIMFGVVICLISVILLGIDGRVY- 531
Db 626 ATLSVVGIALAITFLAFNLHPRKLIKAKLSPPKLSNITAVGCIFYATVILLGLDHSITP 685
QY 532 -SPEEYPKICQARAWLLSTGFTLAYGAMFSKVRVHR-FTTKAKTDPKKVPKLYTMV 589
Db 686 SAEDSFATVCTARVYLLSAGSLAFSGMFAKTYRHRIFTGTGVSFKDMLQDIOILILV 745
QY 590 SGLSIDVILLSWQIFDQRYLETPLDPVSTTD-DIKIRPELHESQORNSMWLGL 648
Db 746 GGLLVALLVTLWVVDPMERHLNLTLE--ISATDRSVYVQVQVEVCRSQHTQWLSV 803
QY 649 VYGFKGILVFLGLAYETRSIKVKQINDSRVGMYSYNNVVLCLITAPVGMVIAQODA 708
Db 804 LYAYKGLLVGVVYMAWETRVKIPALNDSQYIGSVSVVITSVIAVVVLANLISERVTL 863
QY 709 SFAPVALAVIFCCFLSMILLFVPK-----VIEVIRHPKDKAESKYNPDSALSKEDE 759
Db 864 AFITITALITSTATCLLFIPLKHLDIWARNDIIDPVHSMG-LKMECNTRRFVVDORR 922
QY 760 ERYOKLVTEQORLITQKEEKRLVRQRLVERGDAGKTELGATGVASAAVATTSQPA 819
Db 923 ELQYRVEQYRVYKQETQALDAERKL-ERLLESG-----LTTTSTTSSST 968
QY 820 SLINSSAHATPAATFATQ 839
Db 969 SLLTGGGHLKP--ELTVTSG 986

RESULT 8
ID Q23442 PRELIMINARY; PRT; 402 AA.
AC Q23442;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE COSMID ZK180.
GN ZK180.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roope A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Pauley A., Le T.T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58748; AAB52965.1; -.
DR InterPro; IPR00337; GPCR_Mgr.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00003; 7tm3; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

Query Match 10.4%; Score 457; DB 5; Length 402;
Best Local Similarity 29.9%; Pred. No. 1.7e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;
QY 389 ANNSTQFLGVSGVWAFSSOGDRIALQIQEMIDGKYELGYDTQDNLNSWLN--TEQWI 446
Db 15 AIDNSFQGLTGKVRKAN-NERGLVDIKQWSGQVPPFVAVYDGDADDEFKIIDSTTKGW- 72
QY 447 GGVKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFVAFALIIFNINKNHRRVIOSSHPVC 506
Db 73 --SPPLDSITERRRHHISILFLAM-----SLF-----IKMSSPNL 107
QY 507 NTIMLFGVITICLISVILLGIDGRFVSPEYPKICQARAWLLSTGFTLAYGAMFSKVRVHR 566
Db 108 NNIIAGSICTEASVIMGLDTRIVSPDVFVWLCTYKTKWTLCIGFTLSFGAMFSKTRVH 167
QY 567 RTTAKTDPKKVPEWKLYTWVSGLLSIDLVILLSWQIFDPLQRYLETPLDPVSTTD 626
Db 168 SIFTNIRMD-RAIKDSKLFILIGLILFDICVLVTWAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKIRPELHESQORNSMWLGLVYGFKGILVFLGLFAYETRSIKVKQINDSRVGMYSIY 686

Db 223 NTVIPEVEKCNSSHSGVQFVAVLYAVKGVLMILGCLAWETRHVNVPALNDSKYIGTR-- 280
 Qy 687 NVVVLCLITAPVGVWIASQDASFAFVALAVIFCCPL-----SMLLIFVPVKVIEVIRHPDK 743
 Db 281 -----TGDRQVSREV-----FCHFLDNTNVVSRFCADSKSFKTPNFI 319
 Qy 744 AESKYNPDSAISKEDE---ERYOKLVTENEQLORLITQKEKIRVLQRQLVERGDAGKTE 800
 Db 320 MKLFFN-----FSKNSYGGFKNFQKLSFGFNIFARSVQVKKVKVIELARNPV-----GNE 369
 Qy 801 LNG-ATGVASAAVATTSOPAS 820
 Db 370 PRAYERGLMKSVVATTSOPMS 390
 RESULT 9
 Q9V485
 ID Q9V485 PRELIMINARY; PRT; 976 AA.
 AC Q9V485;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE GLU-RA PROTEIN.
 GN GLU-RA OR CG11144.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003846; AAF59402.1; -.
 DR FlyBase; FBgn0019985; Glu-RA.

DR InterPro: IPR001828; ANF_receptor.
 DR InterPro: IPR000337; GPCR_Mgr.
 DR Pfam: PF00003; 7tm_3; 1.
 DR Pfam: PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
 SQ SEQUENCE 976 AA; 108485 MW; 43A0E1F918EDACC4 CRC64;
 Query Match 8.3%; Score 362.5; DB 5; Length 976;
 Best Local Similarity 19.8%; Pred. No. 1.8e-19;
 Matches 202; Conservative 164; Mismatches 384; Indels 281; Gaps 40:
 Qy 3 KDMTSDGAVTFWIFLCL-----IASP-----HLOGGVA-GRPDELHIGGIFPIACKGQWG 53
 Db 2 QKNNNGTILVVMVLSWSRVVDLKSPNTHQDSVSLPGDILGLFPVHEKG---E 58
 Qy 54 GQACMP-----ATRLALDDVKNQPNLLPGFKLILHSNDS----- 87
 Db 59 GAPCGPKVYNRGVORLEAMLYAIDRVNNDPNILPGITIGVHILDTCSRDTVALAQSLOFV 118
 Qy 88 -----ECEPGLGASVMTNLLYNRPDKMLLAGCSTVCTTVAEAAKMNLLIVLC 135
 Db 119 RASLNNDLTSGYECADGSSPOLRKN-ASSGVPFVGIGSYSSVSLQVLANLLRFLHIPQVS 177
 Qy 136 YGASSPALSDRKRPPTLFRTHPSATVHNTRIKLMMKFGSRVAILQQAEEVFISTVDL 195
 Db 178 PASTAKTLSDKTRFDLFARTVPPDTFOSVALVDILKFNWNSYVTHIHEGSGYGEYGEAL 237
 Qy 196 ENRCMEAGVEIVTRQSFSLSDPTDAV-----RNLRRDARIIVGLFVYVAARRVCEMYK 249
 Db 238 HKEATERNVCIATAEKVPSADDDKVEDSIISKLQKPNARGVVLFTRAEDARRIL----- 292
 Qy 250 QQLYGRAHVFFIGWY-EDNMYEVNLAEGI-----TCTVE-QMRTAAE-----GHUTT 296
 Db 293 -QAARLANLSQPFHWIASDGGKQOKLLEGLEADIEAGAITVELQSEIITADRYMMQLTP 351
 Qy 297 E-----ALMW-----NONNOTTISGMTAEERHRLNQAII 326
 Db 352 ETNQRNPFWEYWDNTNCVLTSLSVKPDTSNSANSTDNKIGVRAKTECDSDSYLSEKV- 410
 Qy 327 EEGYDINHRYPEGYQEAPLAY--DAVMSVALAF-----NKTMERLTJTKKSLRDET 376
 Db 411 --GYE-----QESKTOFVVDVAVAFAYALHNLHNDRCNTQSDQTTETRKLQSES 458
 Qy 377 YDKEIADEIYAA-----MNSTQFLGVSG-VVAFSSQGDRIALTQI-- 416
 Db 459 VVYRKISTDTKSOACPDMMANYDGRKEFYNNYLLNVSFIDLAGSEVKFDRQDGLARYDILN 518
 Qy 417 ----EQMIDGKYEKLGYDYDTOLDNLNLSWLTNTQWIGKGPQDRITVTHVLRVSLPLFCVM 472
 Db 519 YQROENSSGYQYKVGKWFNGLQ-----LNSETVVMNKETEQT-----SACSULPEVGM 568
 Qy 473 -----C-----TSSCG-----IF 481
 Db 569 IKKQGGDTCCWICSDCESFEVYDEFTCKDCGPGMLVPADKLSYALDIQYKWNLSLAL 628
 Qy 482 VAFALIIFNI-----WNKHRRYIQSSHPCVNTIMLFGVITICILISVILGIDGRF 530
 Db 629 IPMAIATFGIALTSIVIVLFAKHNHDTPLVRASGRELSYTLFLGILVCYCNFAL----- 682
 Qy 531 VSPPEYFKI--QCARALLSTGFTFLAYGAMFSKVRVRVH-FTTKAKTDPK-KKVEPWKLY 586
 Db 683 ---IAKPTIGSCVLQRFGIGVGFISIYSGALLTKNRISRIEFSKSAQRLKYISPOQSV 739
 Qy 587 TMVSGLLSIDLVILLSQIIFDPLQRYLFTFFLEDPVSTDDIKIRPELEHCEESRNSMWL 646
 Db 740 VITTSLIAQVLITMIWVVEP-----PGTRFYYPDRREVILKCKIQIDMSFLF 787
 Qy 647 GLVYGFKGLIILVFLGLAYETRSIKVKQINDSRVVGMSIYNVWVLCILITAPVGVWIASQ 706

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Db 788 SOLTNM--ILITICTIYAIAKTRKP-ENFNESKFIGFTYTTCIIWLAFVPIYFGTNSY 844
QY 707 DASFAFVALAIFCCFLSMILLIFVPKVEIRHPDKAESKYNPDASISKEDEERYQKLV 766
Db 845 EVQTTICISLSASVALCLYSPKVVILFHP-DKNVKLTMTNSTYRRSAAVAQA 903
QY 767 TENQOLRLITQKEKIRVLRQRLVERGDAGTE-LNG---ATGVASAAVAFTSQP---- 818
Db 904 PTSSGYSRT-----HAPCTSALTGGAVCTNASSSTLPTQNSPHLDE 944
QY 819 ASLINSNAHAT 829
Db 945 ASAQTNVAHKT 955

RESULT 10
Q62916
ID Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U47331; AAA89788.1; -.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR001828; ANF_receptor.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCR_MGR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Query Match 7.98; Score 343.5; DB 11; Length 983;
Best Local Similarity 19.08; Pred. No. 5.6e-18;
Matches 170; Conservative 160; Mismatches 357; Indels 209; Gaps 35;
QY 5 MTSFGAVTFW--IFLLCLIAS-----PHLOGGVAGRP-----DELHIGGIFPIAGK 48
Db 1 MSGKGGWAWMARLPLCLLSLYAPWPSLGGKPKGHPHMSIRIDGDTILGGLFPVHGR 60
QY 49 GWMGGGQAC-----MPATRLADDVYNKPNLIPGFKL----- 80
Db 61 G--SEGRACGLKKEKGIRLEAMLFALDRINNDPDLPLNITLGARILDTCSRDPHALAQ 118
QY 81 -----ILHSNDECEBPGLAGSVMYLLYNKPKMLLAGC--STVCTTVAEAKMWNL 131
Db 119 SLTFVRLALIEKDGTEVRGSGGPP-----ITKPERVGVGASGSSVIMVANILRLFKI 174
QY 132 IVLICYGASSPALSDRKFPITLFRHPNSATVINHPNTRIKLMKFGWSRVAIL-----QQA 184
Db 175 PQISYASTAPDLSNSYDFSFVRVPSDTYQAQAWDVIATKALKNYVSTLASEGYSYSGS 234
QY 185 EEVFISVDELENRCMEAGVEIVTRQSFSLSDPTDAVRLNRQDARIIVGLEFVVAARVRL 244
Db 235 VEAFIQSRENGVCVIAQSKVILPREPTGEPDKIILKLLTNSNAGIILFANEDDIRVL 294
QY 245 CEMYKOOLYGRAHWFFFIGWYEDNW-----YEVNLKAEG-ITCTVPMRIABGHLLT 296
Db 295 EAARRANQTGH---FFWMG--SDSMGSKSAPVLRLEEVAEGAVTILPKRMSVRGDFRYS 349
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QY 297 EALMWNQNTTISGMTAEFRHRLNQAALIEGYDI-----NHDRYPE--GYQE---APLA 347
Db 350 SRTLDNRRNRINWPAEFWEDNFCKLSRHALKKGSHIKCTNRERIGODSAYEGQVQV 409
QY 348 YDAVSVVALAFNKTMTLRTTGKSLRDTFTYDKEIADEIYAAMNSTQFGLGVSQ-VVAFSS 406
Db 410 IDAVYANGHALHAMHRDLCPGRVGL--CPRMDPVDGTQLLKYYIRNVNFSIAGNPVTFE 467
QY 407 QGDRIALTQIEQIDGKYEKLGYDITQLDN-----LSW-----LNTQWIGGKVP 451
Db 468 NGD-----APGRYD---IYQQLRNGSAEYKVGISWTDLHLRIERMQWPGSGQQ 514
QY 452 QDRTIVT-----HVLRT----- 463
Db 515 LPRISCLPCQGERKKTKVKMACCWHCEPCTGYQYQVDRYTKCTCPYDMRPTENRTSCQ 574
QY 464 -----VSLPLFCVCMCTISSCGIFVAFALIIFNWNKHRVYQSSHPVNTIM 510
Db 575 PIPVLEWDSWAVLPLFLAVVGIAT-LFVVVTVFRYN-----DTPIVKASGRELSYVL 629
QY 511 LFGVILCLISVILLGIDGRFVSPPEYKPKICOARAWLLSTGFTLAYGAMFSKYVRVHRTT 570
Db 630 LAGIFLCYATFLM-----IAEPD--LGTCSLRRIFLGLGMSISYAALLTKTRIYRIPE 682
QY 571 KAK--TDPKKKVEPKLYTMVSGLLSIDLVILLSQIFDPLQRYLETFFPLEDPVSTDDI 628
Db 683 QGKRSYSAPRFISPASQALITFILISQLLGLGICWFWDFSHSVVD---FQD--QRTLDP 737
QY 629 KIRPELEHCESORNSMWGLVYGFGLILVFLGFLAYETRSIKVKQINSDRYVGMIIYV 688
Db 738 RFARGVLKCDI--SDLSLCLLGYSMMLMVTCTVYAIKTRGV-ETFNKAKPIGFTMYTT 794
QY 689 VVLCILITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMILLIFVPKVIEVIRH 739
Db 795 CIVWLAFIPI--FFGTQSQADKLIYOTTLTVSVLSASVSGLMYPKVIILFH 848

RESULT 11
Q6QYS2
ID Q6QYS2 PRELIMINARY; PRT; 879 AA.
AC Q6QYS2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN.
GN GRM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=20012997; PubMed=10544282;
RA Mioshima T., Nakanishi S.;
RT "Structural organization of the mouse metabotropic glutamate receptor
RT subtype 3 and its regulation by growth factors in cultured cortical
RT astrocytes.";
RL J. Biochem. 126:889-896(1999).
DR EMBL: AF170701; AAF06741.1; -.
DR EMBL: AF170697; AAF06741.1; JOINED.
DR EMBL: AF170698; AAF06741.1; JOINED.
DR EMBL: AF170699; AAF06741.1; JOINED.
DR EMBL: AF170700; AAF06741.1; JOINED.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR001828; ANF_receptor.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCR_MGR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
```


Db 204 PFSRVVPPDSYQAQAWDIVKALGNVYFILAEGNYSGESVDFAFQVQISREAGGLCIAQS 263
QY 204 VEIVTRQSFSDPT-----DAV--RNLRDARITVGLFVVAARRVCEMYKQOOLYGRAH 257
Db 264 MKIP-----RDPKPGFEFKIIRKLMETPNARGIIFANEDDIKQVLEAARRANLTGH-- 315
QY 258 VWFIFIGWEDNW-----YEVNLKAEGITCTVEQMRIAAG---HLTTEALMWNQN 304
Db 316 -PKFVG--SDSGAKSAPILDNEEV---AEG-AVTILPKRASVEGDFQFTSRSL---EN 365
QY 305 NOTTI--SMTAEERFHRNLQALIE-----EGYD-INHDYRPGYOEAPLAYDAVWS 353
Db 366 NERNWFAEFWEDDFCKLTRPGIKLDPKKCTGERIGRDSPEQEGKVQVDAVYA 425
QY 354 VALAFNKMERUTTGKSLRDFTYTDKEIADEIYAAMNSTQFGLVGV--VAFSSQGDRIA 412
Db 426 MAHALHNHQTCAARGTGLCKMDPVEGRLLSYIRAVN---FNGSAGTGLVFNENGD--- 479
QY 413 LTQIEQMDGKYEKLGYYDTOLDNLS-----WLTNT-- 442
Db 480 -----APGRYDIFQY---QFSNTSSPGYKVIGQSFSISSAKTSSPGYKVFGQWNTNLG 529
QY 443 -----EOWIGGK----- 449
Db 530 INEVEMQWSGGEHYIPASVCFPCOPGERKKMKVGVPCWCHCEPCDGYQYQVGELTCEM 589
QY 450 VPQD-RTIVTHVLRVTS-----LPLFVCMCTISSGFIYAFALIIIFNIWNKH 495
Db 590 CPFDMRPTANHTACTPTPIIKLDHSPWAVPMLAI-----LGAATLSVIVFVREND 644
QY 496 RVIQSSHPVCNTIMLFGV-IICLSVILLGDGRVSPPEYKPKICQARAWLLSTGFTLA 554
Db 645 TPVIRASGRELGYVLTGFLIYLITFLMIA-----EPNTVVCALRLLGLGMCIT 696
QY 555 YGAMFSKVMRVRFTTKAK---TDPKKVPEPKLYTMWCSLLSIDIVILLWSQIFDPQLR 611
Db 697 YSAMLTKTNRIYRIFEQGKKSVTAP-KFISPTSQLVITFVLSQVIGVFIW----- 747
QY 612 YLETPLEDVSTDDIKIR---PELEH---CESQNSMWLGLVYGFKGLIILVFLGLA 664
Db 748 ----FGVPPHTIVDYDELRPNPPELARGILKCDMSDLSLICLSYSI--LLMVTCTVYA 801
QY 665 YETRSIKVQINDSRVGMISYINVVLCILITAPV--GMVIASQODASFAFVALAVIFCCF 722
Db 802 VKSRGVP-ETFEAKPIGTMVTCITVWLAFAVPIFFGTAQSHGEDV----- 846
QY 723 LSMLLIFVPKVEIVIRHPKDKAESKYNPD 751
Db 847 -----HPDDHADRVHEPE 859

RESULT 15
Q98UC5 PRELIMINARY; PRT: 1188 AA.
AC Q98UC5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICED VARIANT B.
GN MGUR5B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Storchmann L.L., Stormann T.M., Parks T.N.;
RT Molecular Cloning and Functional Expression of Chick Metabotropic
RT Glutamate Receptor 5 Splice Variants.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227202; AAK01487.1; -.

KW Receptor. 1188 AA; 132053 MW; 6C179BF8C8045BBD CRC64;
SQ SEQUENCE

Query Match 6.8%; Score 299.5; DB 13; Length 1188;
Best Local Similarity 20.1%; Pred. No. 2.1e-14;
Matches 202; Conservative 153; Mismatches 395; Indels 253; Gaps 40;

QY 16 FLCLIASPHLQGVAGRPDELHGTGGIFPI-----AGKGGWGGQACMPATR 62
Db 20 FGLVSAQANERRVVAHMPGDIIGALFVHHQPTVDKVERKCGVEQYGIQVQEA 79
QY 63 LALDDVKNQNPGLPGFKLILHSND-----SECEPGL-----GA 95
Db 80 HTLDRLNLTPLTNITLGCIEIRDSCHWSAVALQESITFIRDSLISSEEGEVMVRCV 139
QY 96 SVMYNNLYNPKQLMLLAGCSTCTTVAEAAKMNLLVLCYGASSPALSDDKRPETL 155
Db 140 SSSFH--SKPTVGVIGPGSSVAIQONLLQFNIFQIAYSATSMDSKTLKPYMRV 197
QY 156 HPSATVHNPTRIKMKFGMSRVAILOQAAEEVFISTVEDLENRCMEAGVEIVTRQ 215
Db 198 VPSDAQARAMVDIVKRYNMTYVSATVHTEGYSGEAGPKMAAKKEGICIAHSYKI 257
QY 216 PTD-----AVRNLRQ--DARIIVGLFYVAARRVCEMYKQOOLYGRAHVVFI 268
Db 258 AGEQSFDKLLRKLRLSHLPKARVACFCGEMTVRGLLMAMRLRLAGE----- 312
QY 269 WYEVNLKAEGITCIVEQMRIAAG---HLTTEALMWNQNTTISGMT----- 318
Db 313 W-----ADRYDVTGQOREAVGGITIKLQSPDVKWFDYDYLERPETNHRNP 366
QY 319 HRLNQALIEEGYDINHRY-----PEGYQEAFLAY--DAVMSVALAFNKTMERL 365
Db 367 HRFOCL--EGFPOENPKYKNTCTSQMTRLTQHVDQSKMGFVINAIYSMAVGL 424
QY 366 TTGKKSURDFTYDKEI--ADEIYAAMNSTQPLGVSG--VAFSSQGDRIALQI 423
Db 425 CPGVYGLCD---AMKPIDGRKLLESMLKNTFTVSGDMILFDENGDS----- 471
QY 424 YELGYYDTOLDNLSWLNTEQWIGGKVPQDRTIV---THVLRV-SLPL----- 468
Db 472 YEIMNFKMGKDYFDYINVGSWDNGELKMDDEIWESEKNNIIRSVCEPCKEQIK 531
QY 469 -----FVC-MCTISS-----CGIF-----VA 483
Db 532 GEVSCWCTCPCKENYVDFEYTCACQLGSPWDELTCGLDLPVQVLRWGDPEPI 591
QY 484 FALI-----IFNWNKRRVIOSSHPVCNTIMLFGVII-----CLISVILL 527
Db 592 FACLGLLATLVTAIFIMYRDTVPVKSRSREL--YIILAGICLGLYCTFCU 643
QY 528 GRFVSPEEYKICQARAWLLSTGFTLAYGAMFSKVMRVRHRETTAKTDPKKV 587
Db 644 ----KPOOI---YCYLQIGIGLSPAMSTYSALVTNTRIARILAGS----- 693
QY 588 MVSGLLSIDLWILLWSQIFDPLQRYLETFFPLEDPVSTDDIKIRPELHCESES 647
Db 694 MSACQALVIAFILICIQ----LGIIVAFIMEPPDIMHDYPSIREVYLIC---- 745
QY 648 LV--YGFKGLILVFLGLFLAYETRSIKVQINDSRVGMISYINVVLCILITAP 705
Db 746 VVTPGLYNGLLILSCTFYAFKTRNVPA--NFNEAKYIAFTMTTTCIILWAFVPI 797
QY 706 QDASFAFVALAVIFCCF-----LSMLLIFFVPKVIEWIRHPKDKAESKYNPD 754
Db 798 ----YFGSNKYKIITMCFVSLSATVLCGMFVPKVYIILAKPERNVRSATFT 853
QY 755 ----SKEDERYQKLV-----TENEOL----ORLTQKEKIRVLRQRLVERG 799
Db 854 GDGKSSAAASRSSSLVNLWKRKRGSGETLYKGRRLAPHKSE-----IEC 904
QY 800 ELNG--ATGVASAAVATTSQPSALINSAAHTAATLAITQGE 840

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Db 905 MNGGRATWTSSNGKSYSWAQNEKSSRG AHLWQRLSIHINKKE 947
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